Influenza and the One Health Approach

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Duke Kunshan University
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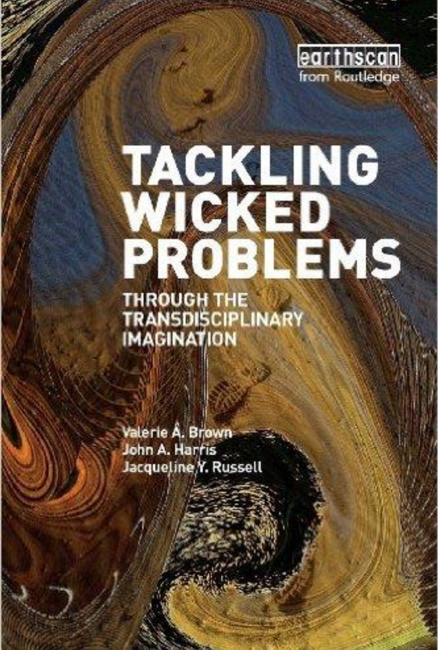
Kunshan, Jiangsu, China

Outline

- The One Health concept
- Trends in the One Health
- Influenza and One Health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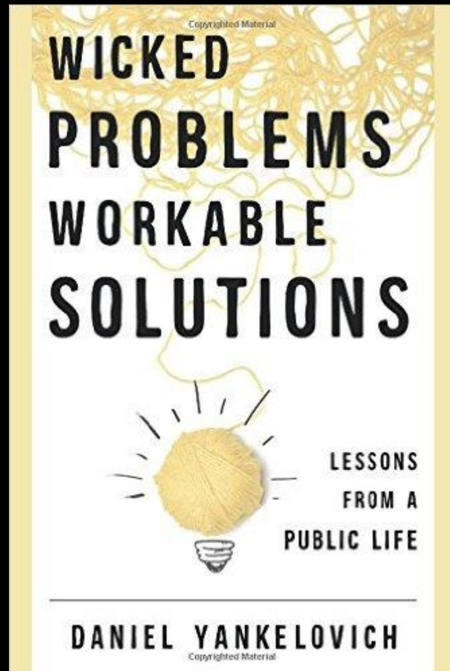
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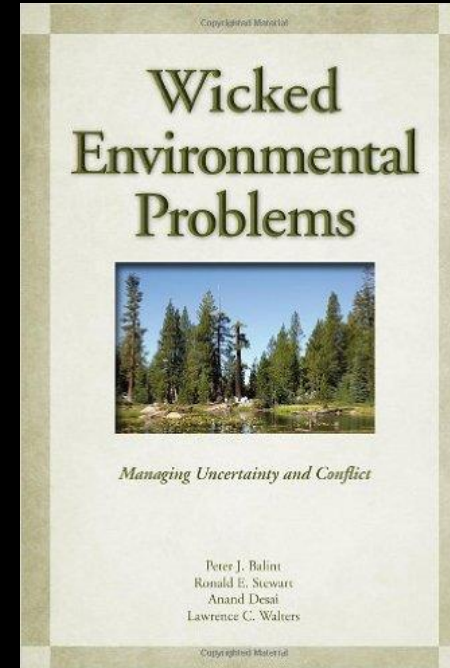
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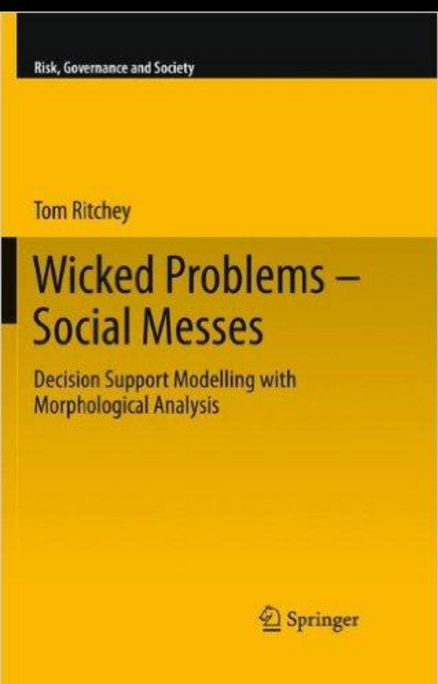
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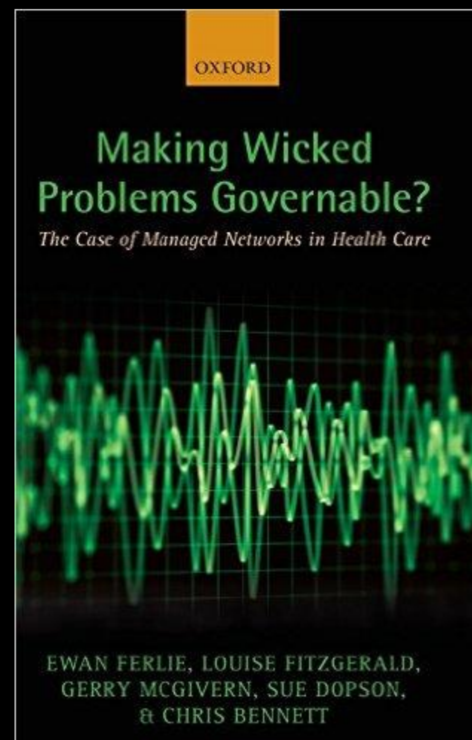
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The Case of Managed Networks in Health Care
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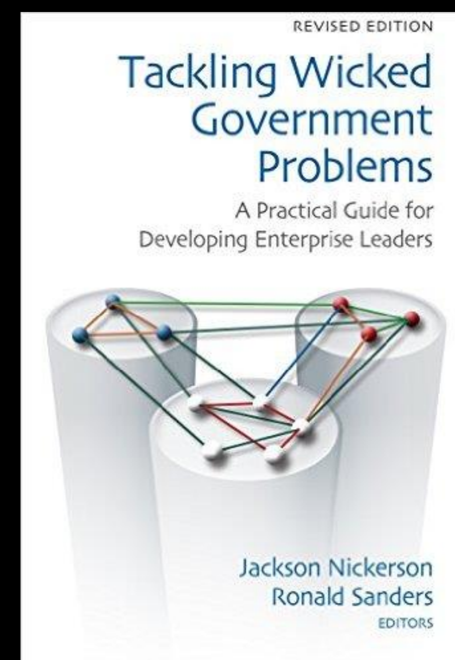
& CHRIS BENNETT

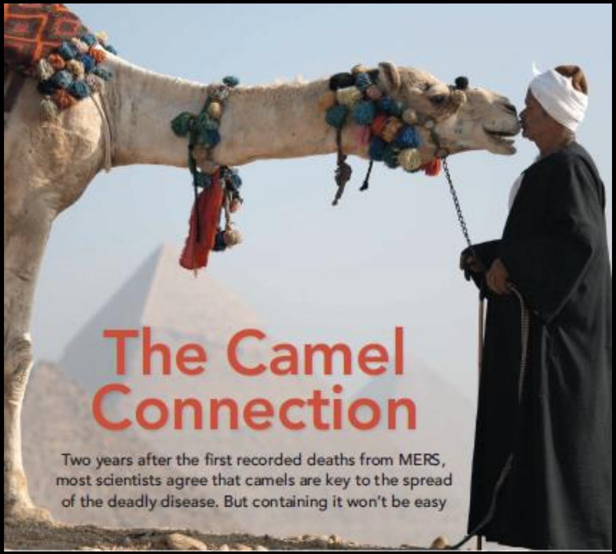

REVISED EDITION
Tackling Wicked Government Problems
A Practical Guide for Developing Enterprise Leaders
Jackson Nickerson
Ronald Sanders
EDITORS

Tackling Wicked Problems from the Australian Public Service Commission:

- Wicked problems have many interdependencies and are often multi-causal – there may be conflicting goals for those involved
- Attempts to address wicked problems often lead to unforeseen consequences – wicked problems exist in complex systems that exhibit unpredictable, emergent behavior
- Wicked problems are often not stable – understanding of the problem is constantly evolving
- Wicked problems usually have no clear solution – there is no right or wrong response, although there might be worse or better responses
- Wicked problems hardly ever sit conveniently within the responsibility of any one organization – these problems cross governance boundaries

Humans as Sentinels of Emerging Zoonotic Disease Spread

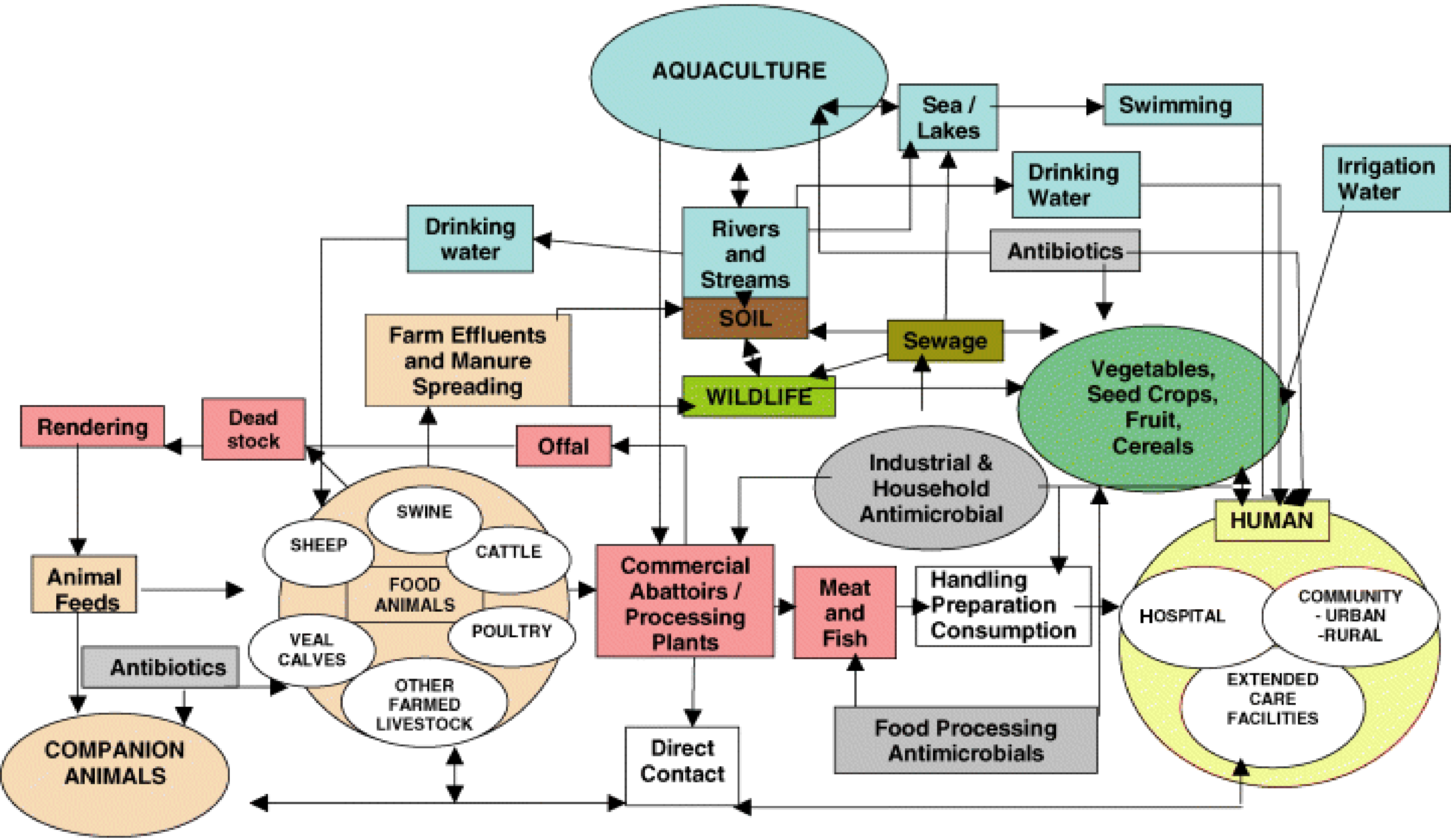
H7N9 influenza



MERS-CoV

H3N2v influenza

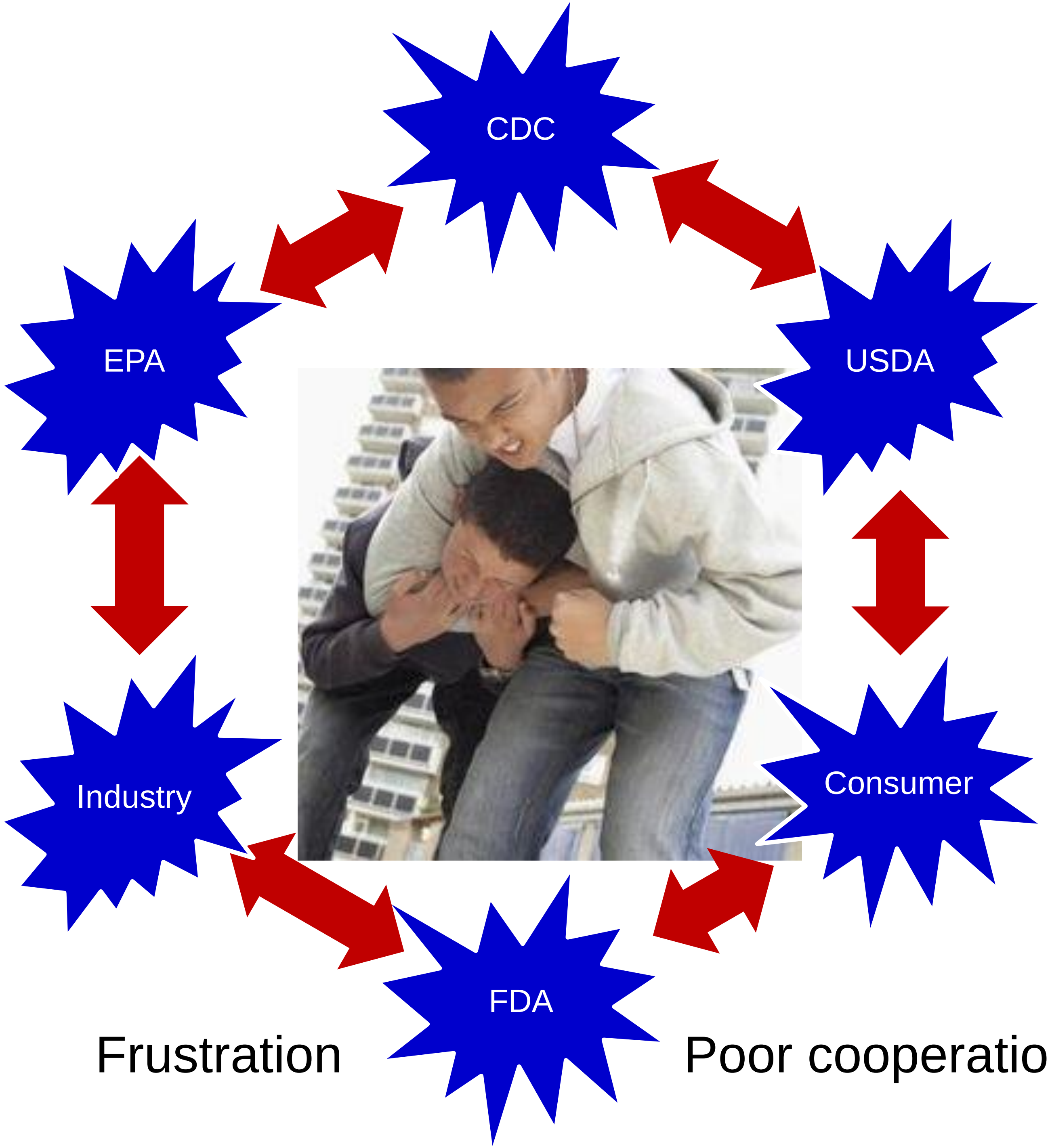
Antimicrobial Resistance: Implications for the Food System



Comprehensive Reviews in Food Science and Food Safety
Volume 5, Issue 3, pages 71-137, 2 AUG 2006 DOI: 10.1111/j.1541-4337.2006.00004.x
http://onlinelibrary.wiley.com/doi/10.1111/j.1541-4337.2006.00004.x/full#f1


The Well-Traveled Salad.
Do You Know Where Your Food Has Been?
As consumers, many of us fail to recognize that even our domestic and local food supplies are part of a global network. The daily activity of consuming food directly links our health as humans to the health of crops and produce, food animals, and the environments in which they are produced.
LETTUCE
Canada, Chile, Dominican Republic, Mexico, Peru, USA
CUCUMBERS
Canada, Honduras, India, Mexico, Spain, USA
FETA CHEESE
Canada, Denmark, Egypt, Germany, Greece, Israel, Italy, Turkey, UK, USA
VINAIGRETTE
Argentina, Brazil, Canada, Chile, China, France, Germany, Greece, India, Indonesia, Italy, Mexico, Morocco, Peru, Portugal, Spain, Thailand, Tunisia, Turkey, USA, Vietnam
OLIVES
Greece, Israel, Mexico, Spain, USA
SPROUTS
Argentina, Australia, Bangladesh, Canada, China, Egypt, France, India, Morocco, Nepal, Pakistan, South Africa, Spain, Turkey, USA
MANDARIN ORANGES
Israel, Mexico, Morocco, South Africa, Spain
ONIONS
Canada, China, Germany, India, USA
TOMATOES
Canada, Dominican Republic, Holland, Israel, Italy, Mexico, USA
CROUTONS
Argentina, Australia, Brazil, Canada, China, France, India, Mexico, Netherlands, Poland, Russia, Switzerland, Uruguay, USA, Vietnam
A "One Health" approach to food safety—bringing together expertise and resources from the clinical, veterinary, wildlife health, and ecology communities—has the potential to reveal the sources, pathways, and factors driving the outbreaks of foodborne illness and possibly prevent them from occurring in the first place.
NOTE: Countries are listed in alphabetical order and not by volume of export.
INSTITUTE OF MEDICINE
OF THE NATIONAL ACADEMIES
www.iom.edu

- No one discipline is trained to engage such complex public health problems
- No one agency or organization can control such problems



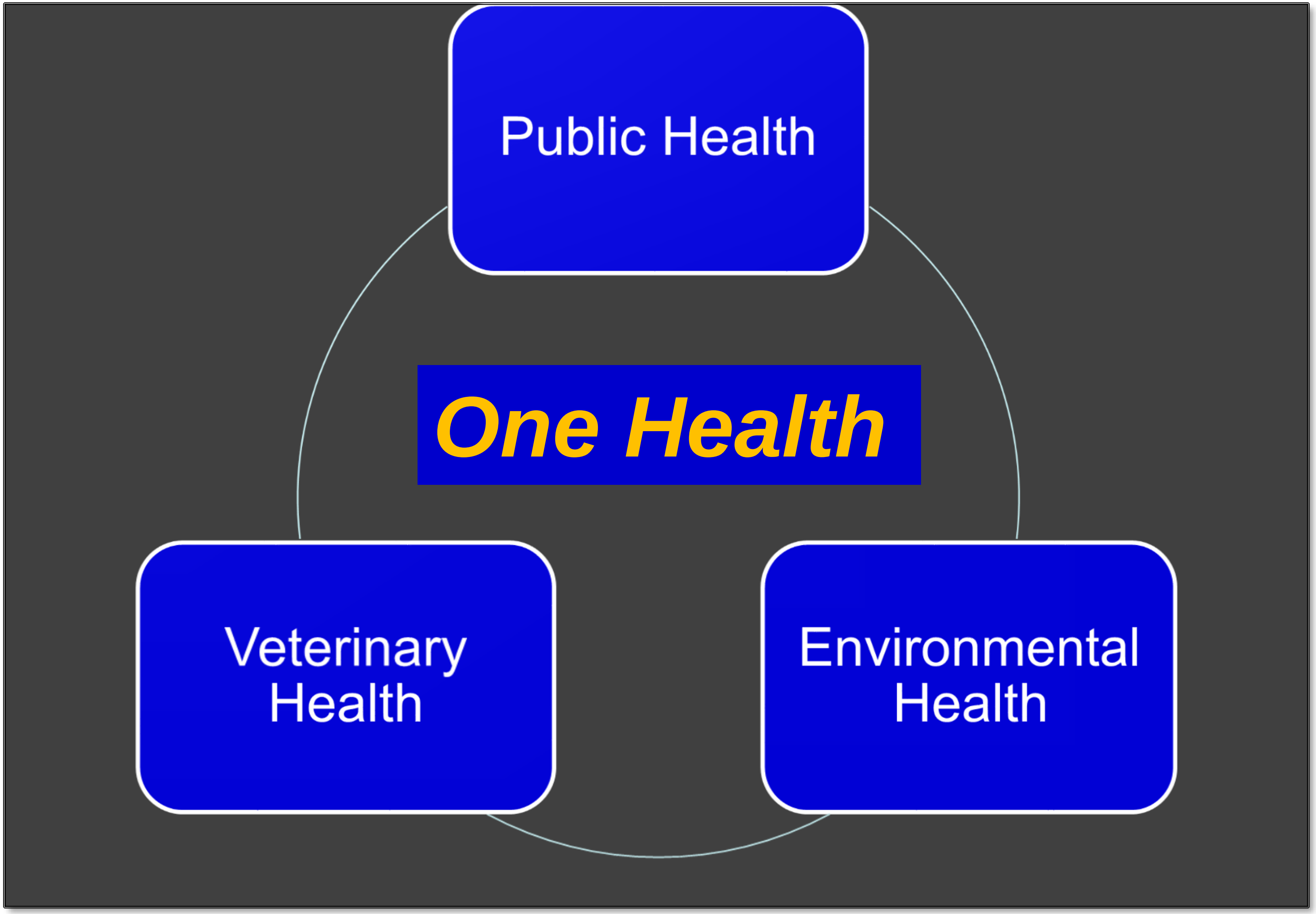
Frustration

Poor cooperation

One Health Defined

"One Health is the collaborative effort
of multiple disciplines
- working locally, nationally, and globally -
to attain optimal health
for people, animals, and our environment."

AVMA One Health Initiative Task Force 2008



A One Health approach gains cooperation from all parties involved and employs public health, veterinary health, and environmental health approaches to bring balance to solving difficult public health problems

Confronting Complex Public Health Problems: The Development of Interdisciplinary Research

David R. Holmes
Journal of Public Health Policy
Vol. 2, No. 4 (Dec., 1981), pp. 361-381

Published by: Palgrave Macmillan Journals
DOI: 10.2307/3342477
Stable URL: http://www.jstor.org/stable/3342477
Page Count: 21

"…Interdisciplinary research (in contrasts to multi-disciplinary research)…is more team-oriented, and its primary distinguishing features are a shared definition of the problem that permeates the total research process and a final product which blends the various contributions so that neither the identity nor the disciplinary background of the individual authors can be determined…. the research team jointly structures the problem and draws on appropriate tools and techniques from each of their fields, sometimes inventing new methods to cope with those questions which inevitably will cross disciplinary lines."

Selection of Organizations that have Endorsed the One Health Initiative as of July 2015

Agronomes et Vétérinaires Sans Frontières (AVSF)
American Academy of Family Physicians
American Academy of Pediatrics
American Association of Public Health Physicians (AAPHP)
American Association of Veterinary Laboratory Diagnosticians
American Association of Wildlife Veterinarians
American College of Preventive Medicine (ACPM)
American College of Veterinary Microbiologists
American College of Veterinary Pathologists
American College of Veterinary Preventive Medici
American Medical Association
American Mosquito Control Association (AMCA)
American Nurses Association
American Physiological Society
American Phytopathological Society
American Society for Microbiology
American Society of Tropical Medicine and Hygien
American Veterinary Medical Association
Animal Medical Center, New York (USA)
Animal/Human Health for Environment and Development for Great Limpopo Transfrontier Conservation Area
Association of Academic Health Centers
Association of American Medical Colleges
Association of American Veterinary Medical Colleg
Association of Schools of Public Health
Auburn University's College of Veterinary Medicin Auburn, Alabama (USA)
Bella Moss Foundation, United Kingdom
Biomedical Technology, Epidemiology and Food Sa Global Network: Brno, Czech Republic
CAB International (CABI) http://www.cabi.org
CGIAR Research Program – Agriculture for Nutritio and Health (A4NH)
College of Veterinary Medicine and Biomedical Sciences, Texas A&M University (USA)
Conservation through Public Health (CTPH) - http://www.ctph.org/index.php
Corporation Red SPVet, Bogota-Columbia
Council for Agricultural Science and Technology (C
Council of State and Territorial Epidemiologists
Croatian Society for Infectious Diseases
Delta Society
Department of Molecular and Comparative Pathobiology, Johns Hopkins University School of Medicine
Exuberant Animal
Faculty of Veterinary Medicine at the Universidad Autonoma de Nuevo Leon, Mexico
Federation of Veterinarians of Europe (FVE)
Global Alliance for Rabies Control
Horizon International, Yale University
Immune Macro Biotic Technology (IMBT), UK
Immuno Valley Consortium in The Netherlands
Indian Veterinary Public Health Association
Infection Prevention and Control (IPAC Canada)
Institute of Tropical Medicine, Department of Anir Health, Antwerp, Belgium
Interacademy Medical Panel (IAMP)
International Journal of One Health (India)
International Livestock Research Institute (ILRI)
Italian Society of Preventive Medicine
Kansas City Area Life Sciences Institute – Kansas Ci MO (USA)
National Academies of Practice (NAP)
National Association of State Public Health Veterinarians
National Centre for Animal Health, Bhutan
National Environmental Health Association (NEHA
National Forum of Comparative Medicine (Romani Academy of Medical Sciences)
National Park Service (USA)
New Zealand Centre for Conservation Medicine (NZCCM) - Auckland
Nigerian Biomedical and Life Scientists
Nigerian Veterinary Medical Association
One Health Commission - USA
One Health in Epidemiology, Massey University, N Zealand
One Health New Medical Concept Association in Romania
Ovarian Cancer Symptom Awareness (OCSA) - USA
Praecipio International
SAPUVET III Project
Silent Heroes Foundation
Society for Tropical Veterinary Medicine
South Africa Society of Travel Medicine (SASTM)
SpayFIRST, Inc.
State Environmental Health Directors
United States Animal Health Association (USAHA)
Urban Health and Climate Resilience Centre - Sura India
Veterinarians without Borders/ Vétérinaires sans Frontières - Canada
Veterinarni Medicina, the international journal for biomedical and veterinary sciences http://vetmed.vri.cz/
Veterinary Bioscience Institute
Volunteers for Intercultural and Definitive Adventu (VIDA) - www.vidavolunteertravel.org
WiLDCOAST/COSTASALVAjE http://www.wildcoast.net/
Wildlife Disease Association
World Association of Veterinary Laboratory Diagnosticians
World Medical Association
World Organization of Family Doctors (WONCA)
Zoonotic and Emerging Diseases, Edinburgh, U

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One Health Commission

Cheryl Stroud, DVM, PhD

World Health Through Collaboration

WHY ONE HEALTH? | LEADERSHIP | SPONSORS | ONE HEALTH NEWS | COMMISSION NEWS | EVENTS/CALENDAR | RESOURCES

See 'What' we are doing

"CONNECT" - One Health Stakeholders to

"CREATE" - Strategic Networks/Teams/Partnerships that will

"EDUCATE" - About One Health issues.

OH Public Service Announcement

Bat Rabies Posters

1st Int'l Who's Who in OH Webinar

OHC Action Teams

OHC Letter to The White House

more »

Support The Commission

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Become a sponsor of the One Health Commission. Apply your passion and skills to improving the health of humans, animals, plants and the environment.

Sponsorship opportunities

Support the Commission by registering through:

Students for One Health

STUDENT One Health Initiatives

STUDENT Listserv Sign-up

STUDENT One Health FACEBOOK Page

STUDENT Future Leaders in One Health LinkedIn Page

One Health in the News

07/13/15 Extraordinary One Health Leader Awarded Gold Headed Cane (USA): an internationally recognized physician virologist and vaccine developer

Dr. Thomas P. Monath [MD, FACP,...

07/02/15 OIE Press release: Public health, animal health and security sector must speak with one voice on the need to

One Health Hot Topics

**** HOT TOPICS ****

WHO report urging action on Neglected Zoonotic Diseases. Chapter 2 focuses on "The value of intersectoral working - One Health"

Seven US Senators send One Health Congressional Letter to White House, February 2015

Now nearly 2000 “One Health” citations in PUBMED as if 12/8/15

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PubMed | "One Health"

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Emerging Viral Diseases: The One Health Connection: Workshop Summary.

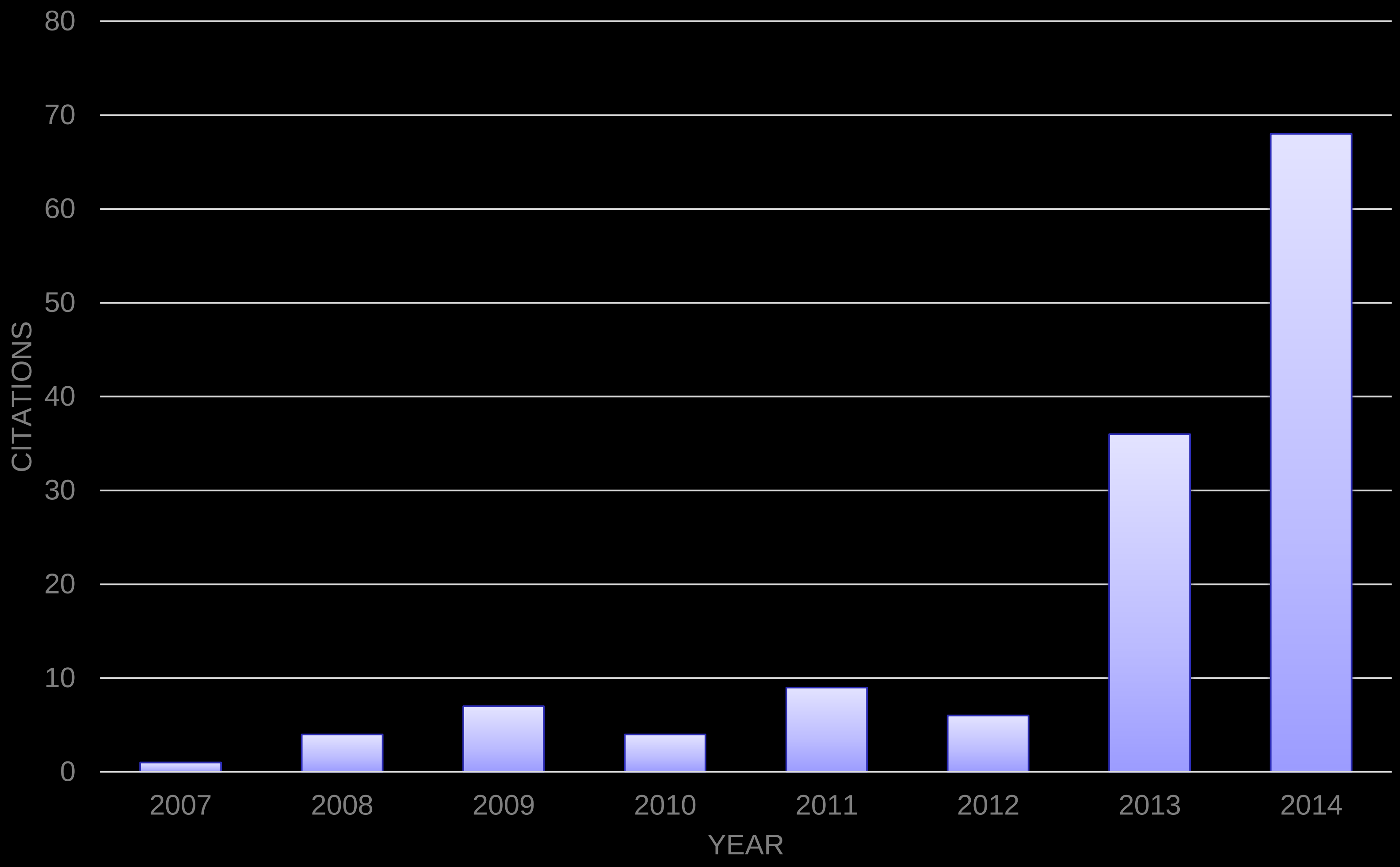
Forum on Microbial Threats; Board on Global Health; Institute of Medicine.

Washington (DC): National Academies Press (US); 2015 Mar.
The National Academies Collection: Reports funded by National Institutes of Health.

Excerpt

In the past half century, deadly disease outbreaks caused by novel viruses of animal origin — Nipah virus in Malaysia, Hendra virus in Australia, Hantavirus in the United States, Ebola virus in Africa, along with HIV (human immunodeficiency virus), several influenza subtypes, and the SARS (sudden acute respiratory syndrome) and MERS (Middle East respiratory syndrome) coronaviruses — have underscored the urgency of understanding factors influencing viral disease emergence and spread. *Emerging Viral Diseases* is the summary of a public workshop hosted in March 2014 to examine factors driving the appearance, establishment, and spread of emerging, re-emerging and novel viral diseases; the global health and economic impacts of recently emerging and novel viral diseases in humans; and the scientific and policy approaches to improving domestic and international capacity to detect and respond to global outbreaks of infectious disease. This report is a record of the presentations and discussion of the event.

One Health Research Publications



PUBMED search 9/19/15 for “One Health initiative” or “One Health approach” in abstract or title by year

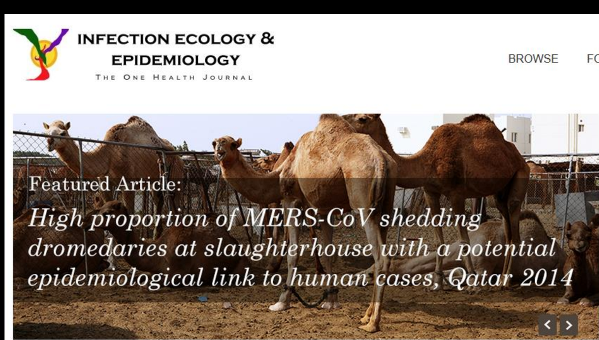
One Health Journals

Infection Ecology and Epidemiology The One Health Journal (Sweden)
http://www.infectionecologyandepidemiology.net/index.php/iee

EcoHealth
http://www.springer.com/public+health/journal/10393

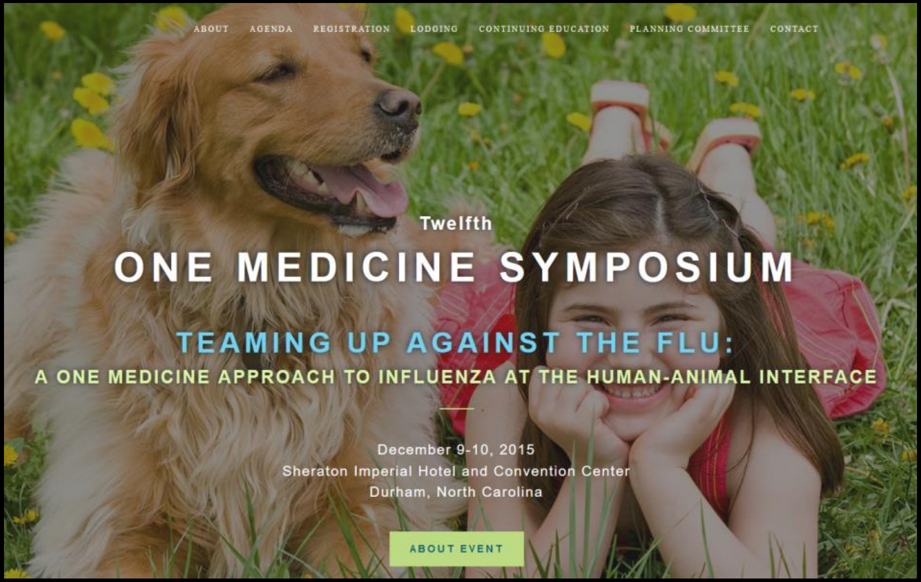
International Journal of One Health (India)
http://www.onehealthjournal.org/

One Health Official Journal of the One Health Foundation
http://www.journals.elsevier.com/one-health



Abstracted from http://www.onehealthinitiative.com/journals.php Aug 20, 2015

One Health Conferences



Agencies which have funded or are planning to fund One Health research or training grants
Gates Foundation USAID EPT-2 Program ($300M) World Bank US Department of Defense Global Emerging Infections Surveillance US State Department US Department of Homeland Security US Defense Threat Reduction Agency (STEP) ($120M) US NIH National Institute of Allergy and Infectious Diseases US NIH Fogarty International Center UK Research Council UK Department of International Development

Are there Job Opportunities in One Health?

- One Health postdoc Kunshan China (now x 2 yrs)
- One Health postdoc D43 Ulaanbaatar, Mongolia (May 2016 x 2 yrs)
- One Health Masters study coordinator Duke University (now)
- One Health Masters study coordinator Duke-NUS Singapore (now)

One Health Training

U. S. universities promoting One Health programs

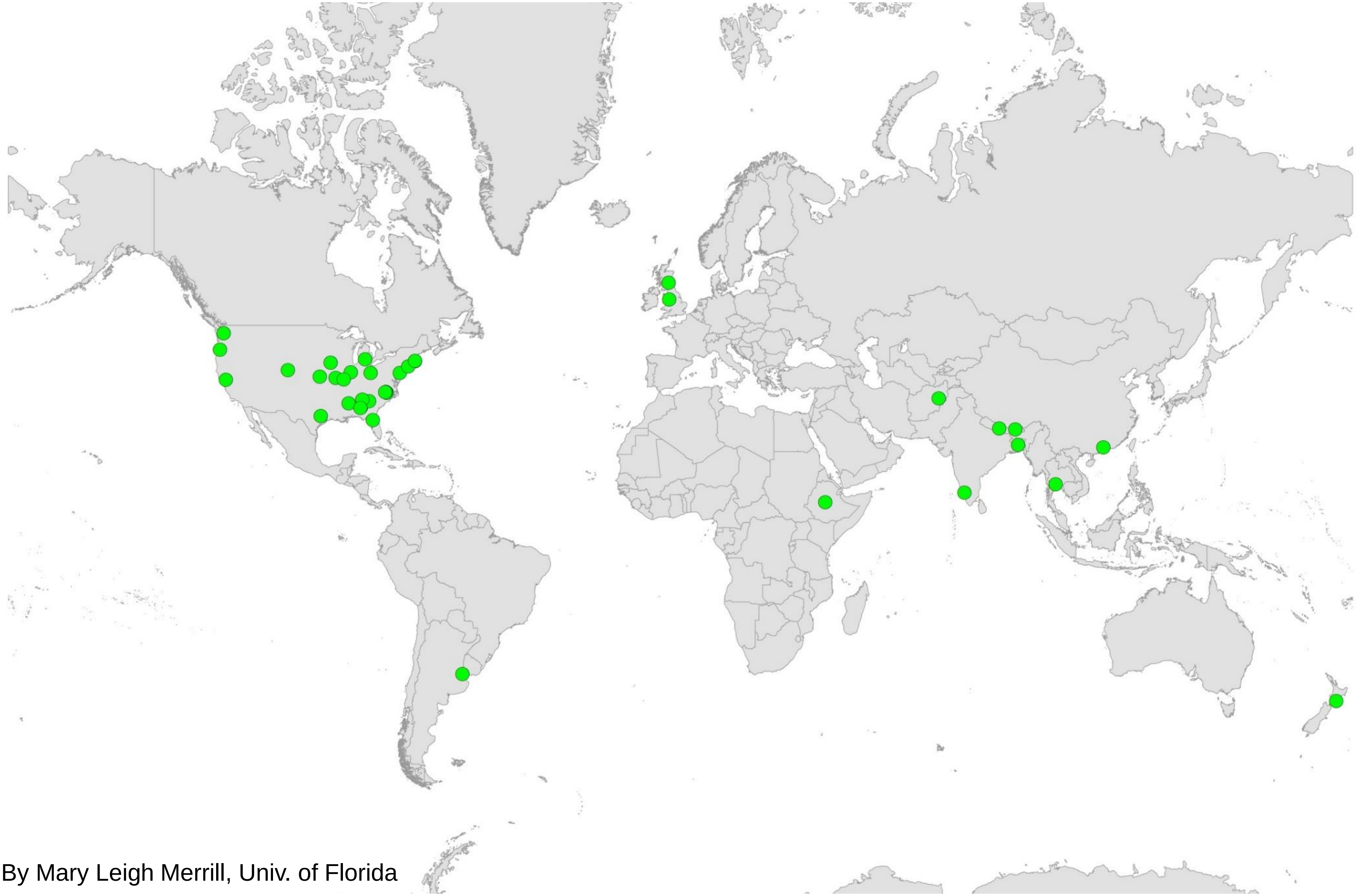
By Mary Leigh Merrill, Univ. of Florida

One Health and Academic Institutions

- 51 academic institutions have some sort of a One Health program
- 9 institutions have certificate, masters, or PhD programs in One Health

From a WWW search Aug 2015

Universities Around the World with One Health Programs (as of June 2014)



By Mary Leigh Merrill, Univ. of Florida

North Carolina One Health Collaborative

We can be found at:

- Home
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- About The Collaborative
- IEG Lecture Series
- Course Offering
- One Health News
- Additional Resources
- Events
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One World, One Health

The One Health discussion series is open to the public and brings together public health professionals, physicians, veterinarians, environmental researchers and other global health professionals to discuss current research relevant to One Health issues. The Intellectual Exchange Group Series is available to professional and graduate students who wish to participate for credit. The spring semester course is cross-listed at Duke, UNC, and NC State.

Course Overview

This interdisciplinary course will introduce the concept of One Health as an increasingly important approach to a holistic understanding of disease prevention and the maintenance of human and animal health. The list of topics will include a discussion of bidirectional impact of animal health on human health, the impact of earth's changing ecology on health, issues of food and water security and preparedness, and the benefits of comparative medicine.

Course Objectives

Students will be able to

1. Describe how different disciplines contribute to the practice of One Health.
2. Discuss how interdisciplinary interventions can improve

Course Blog

For more information, please contact:

Duke: Chris Woods chris.woods@duke.edu
UNC: Mamie Sackey Harris, msharris @med.unc.edu
NC State: Suzanne Kennedy-Stoskopf, suzanne_stoskopf@ncsu.edu

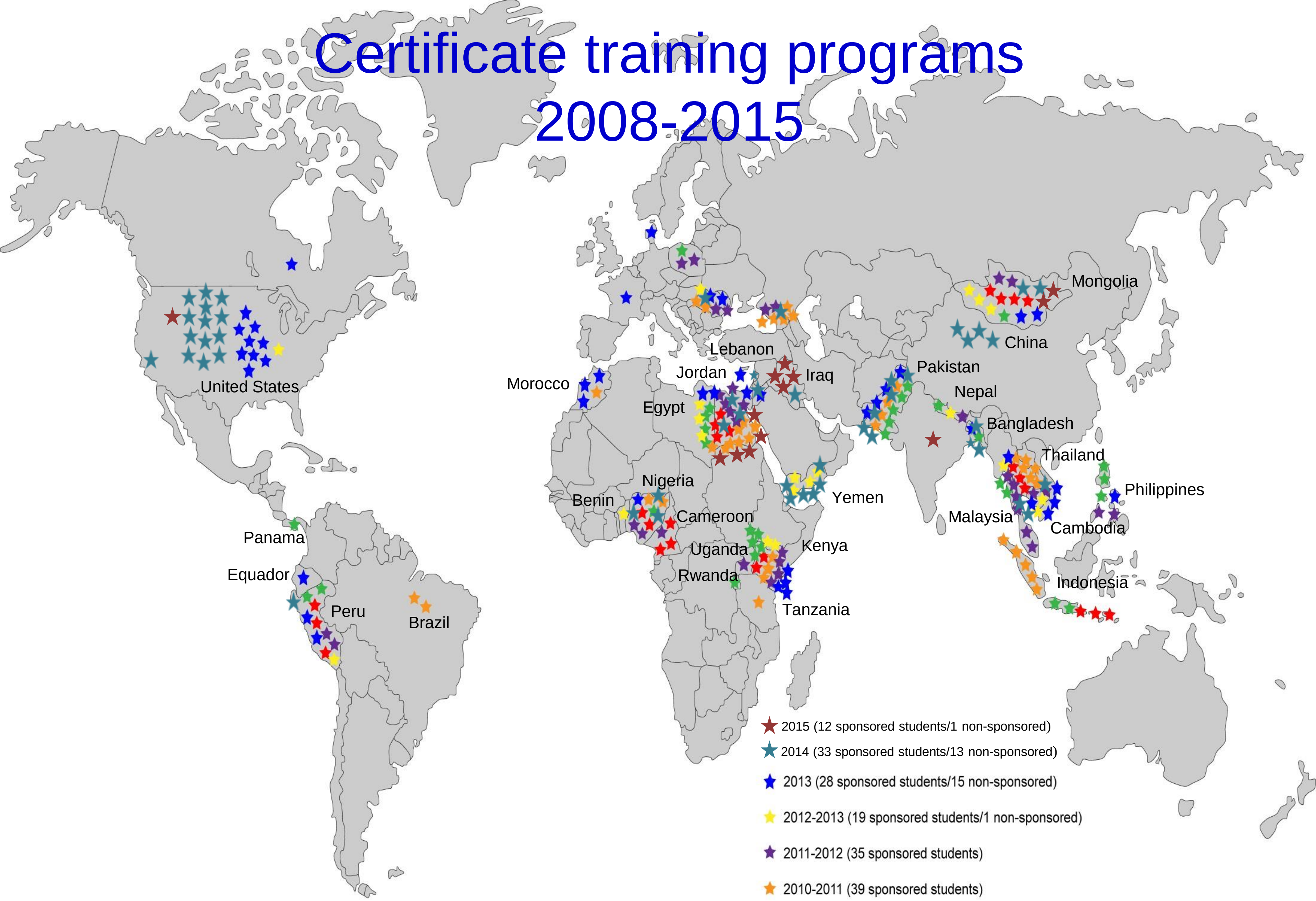
One Health Training Program

4 graduate courses at Duke during May (3 wks)

- An Introduction to One Health Problem Solving (2 credits)
- Public Health Laboratory Techniques (1 credit)
- An Introduction to Entomology Zoonotic Diseases & Food Safety (3 credits)
- Introduction to Environmental Health (3 credits)



Certificate training programs 2008-2015

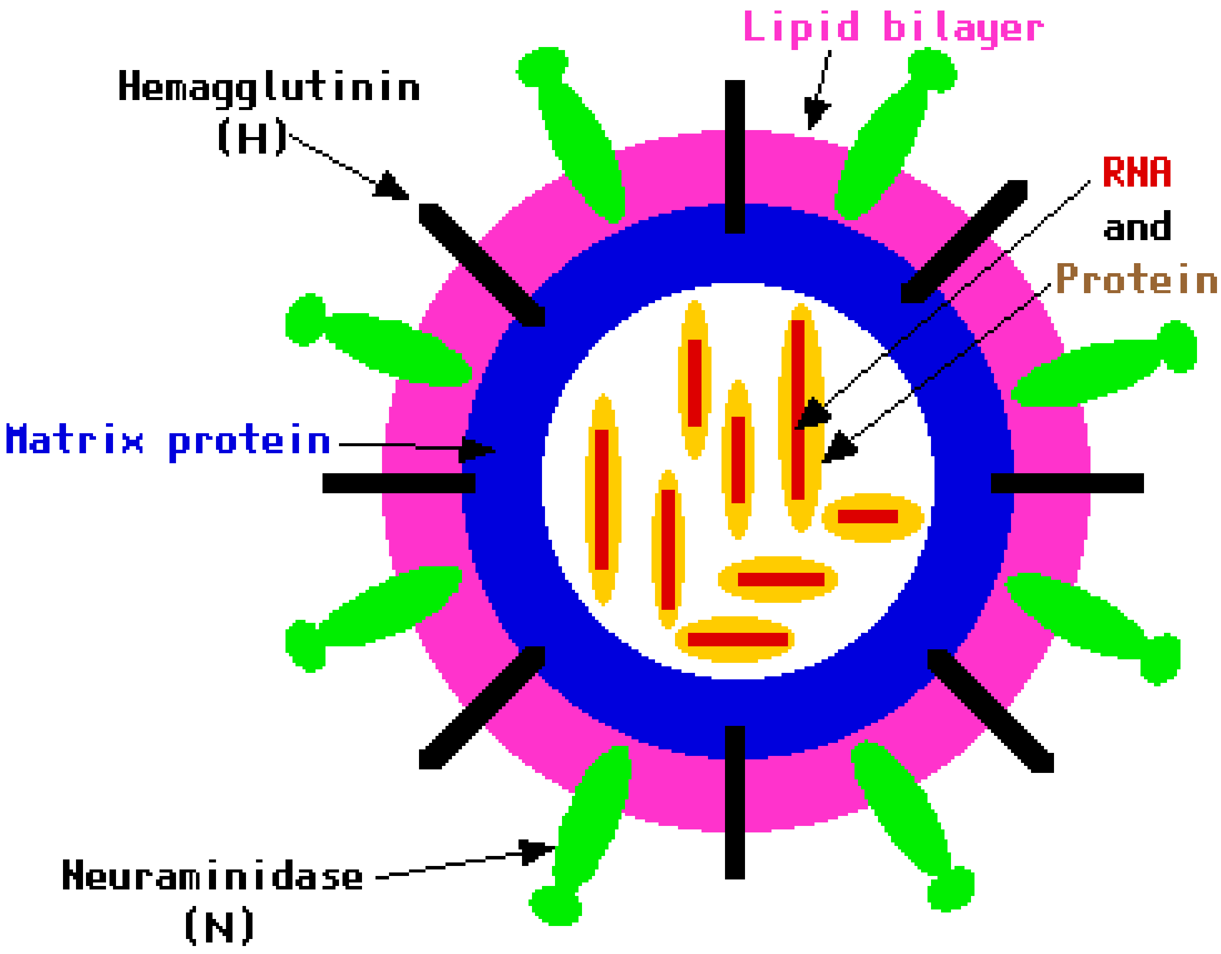


One Health and Influenza

Influenza Viruses

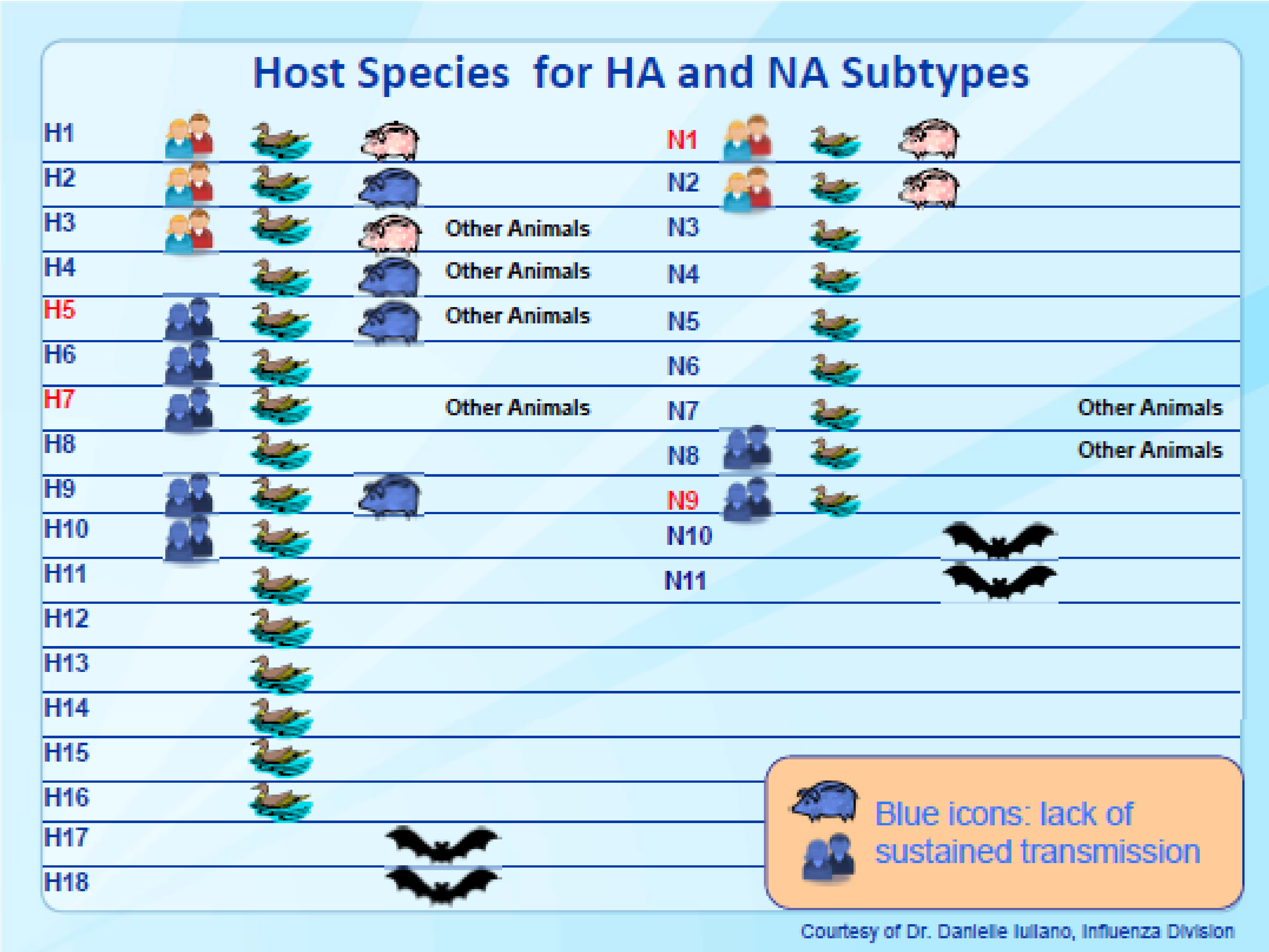
- Type A
  - *Humans, domestic and wild animals*
- Type B
  - *Humans, pigs, seals*
- Type C
  - *Humans, pigs (mild disease in man)*
- Type D
  - *Cattle, pigs, goats, sheep, humans (mild disease in man)*

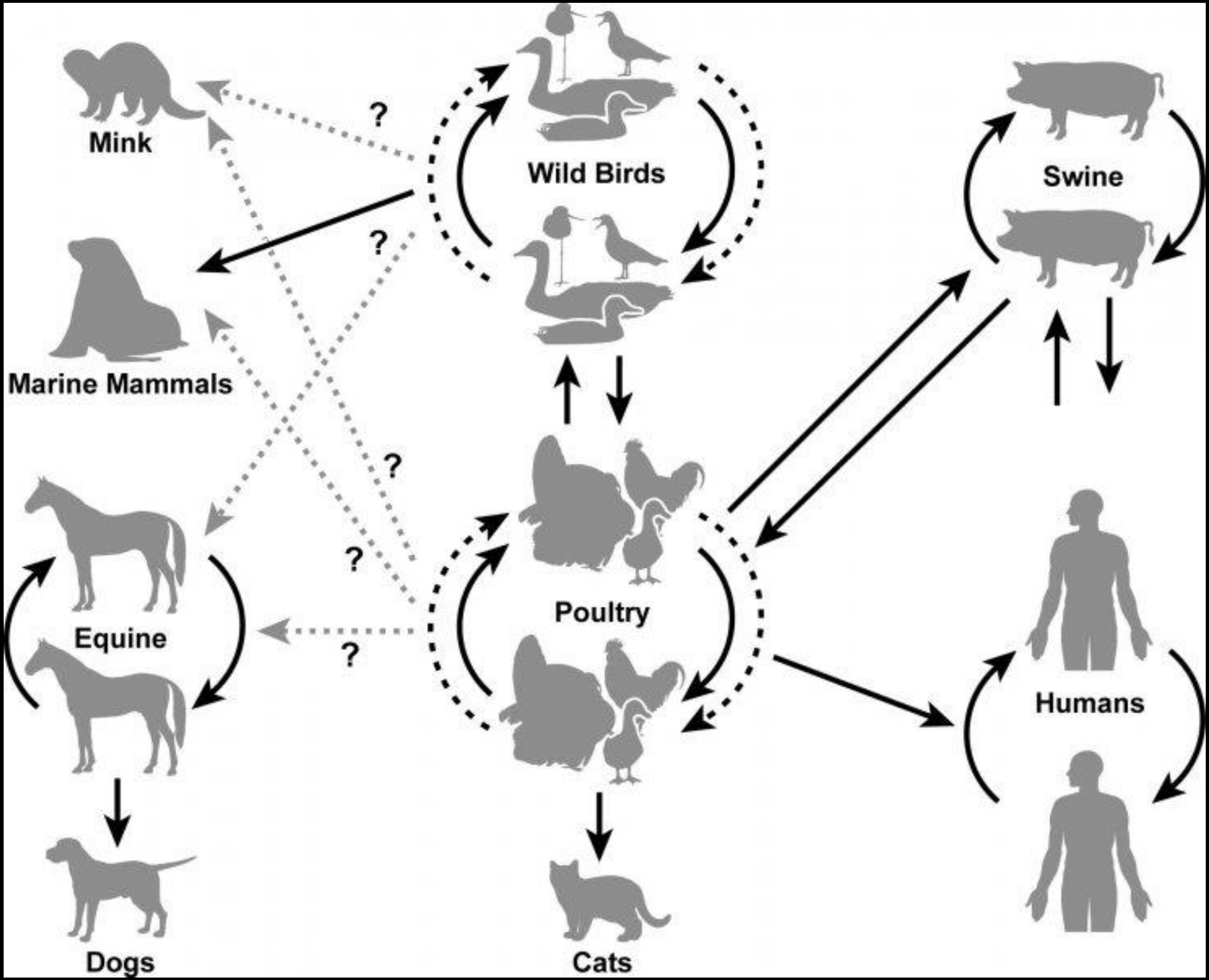
18 H types – types 1, 2, and 3 in man



11 N types – types 1 & 2 found in man

From www.ultranet.com/~jkimball/BiologyPages/ F/FluVirion.gif


Host Species for HA and NA Subtypes
H1
H2
H3
Other Animals
H4
Other Animals
H5
Other Animals
H6
H7
Other Animals
H8
H9
H10
H11
H12
H13
H14
H15
H16
H17
H18
N1
N2
N3
N4
N5
N6
N7
Other Animals
N8
Other Animals
N9
N10
N11
Blue icons: lack of sustained transmission
Courtesy of Dr. Danielle Iuliano, Influenza Division



From http://vet.osu.edu/preventive-medicine/aieerp-background-information-animal-influenza

Found first evidence that camels may play a role in the ecology of equine influenza

Equine Influenza A(H3N8) Virus Isolated from Bactrian Camel, Mongolia

Myagmarsukh Yondon, Batsukh Zayat, Martha I. Nelson, Gary L. Heil, Benjamin D. Anderson, Xudong Lin, Rebecca A. Halpin, Pamela P. McKenzie, Sarah K. White, David E. Wentworth, and Gregory C. Gray

Because little is known about the ecology of influenza viruses in camels, 460 nasal swab specimens were collected from healthy (no overt illness) Bactrian camels in Mongolia during 2012. One specimen was positive for influenza A virus (A/camel/Mongolia/335/2012[H3N8]), which is phylogenetically related to equine influenza A(H3N8) viruses and probably represents natural horse-to-camel transmission.

Since the first isolation in 1963 of an avian-origin influenza A(H3N8) virus from horses (*1*), subtype H3N8

A/PR-8/34 + A/USSR/77, generated in a Soviet lab tory and administered to humans in Mongolia and sibly transmitted from vaccinated humans to camels reactivated form (*5*,*6*). However, only 1 genetic sequ from this outbreak among camels is available in Bank: A/camel/Mongolia/1982/H1N1. Despite repor serologic activity against influenza A virus among ca in several African countries (*7*,*8*), the lack of isolate rus from these populations highlights how little is known about the ecology of influenza viruses in camels. Questions about the potential role of camels in human cases of Middle East respiratory syndrome (*9*) further highlight our lack of knowledge of infectious diseases in camels and the merits of increased surveillance at this unique human–animal interface.

Since January 2011, surveillance of equine influenza viruses has been enhanced in 3 Mongolian aimags (provinces). Surveillance among camels was also initiated in response to anecdotal reports of signs of respiratory illness in Bactrian camels (*Camelus bactrianus*). We describe the isolation, full-genome sequencing, and phylogenetic characterization of an influenza A(H3N8) virus of equine lineage isolated from a Bactrian camel, thereby identifying a novel route of influenza virus interspecies transmission and raising further questions about influenza A virus ecology in understudied regions such as Mongolia.

Emerging Infectious Diseases • www.cdc.gov/eid • Vol. 20, No. 12, December 2014

Minimizing Novel Influenza Generation and Spread in Modern Agriculture is a Wicked Problem

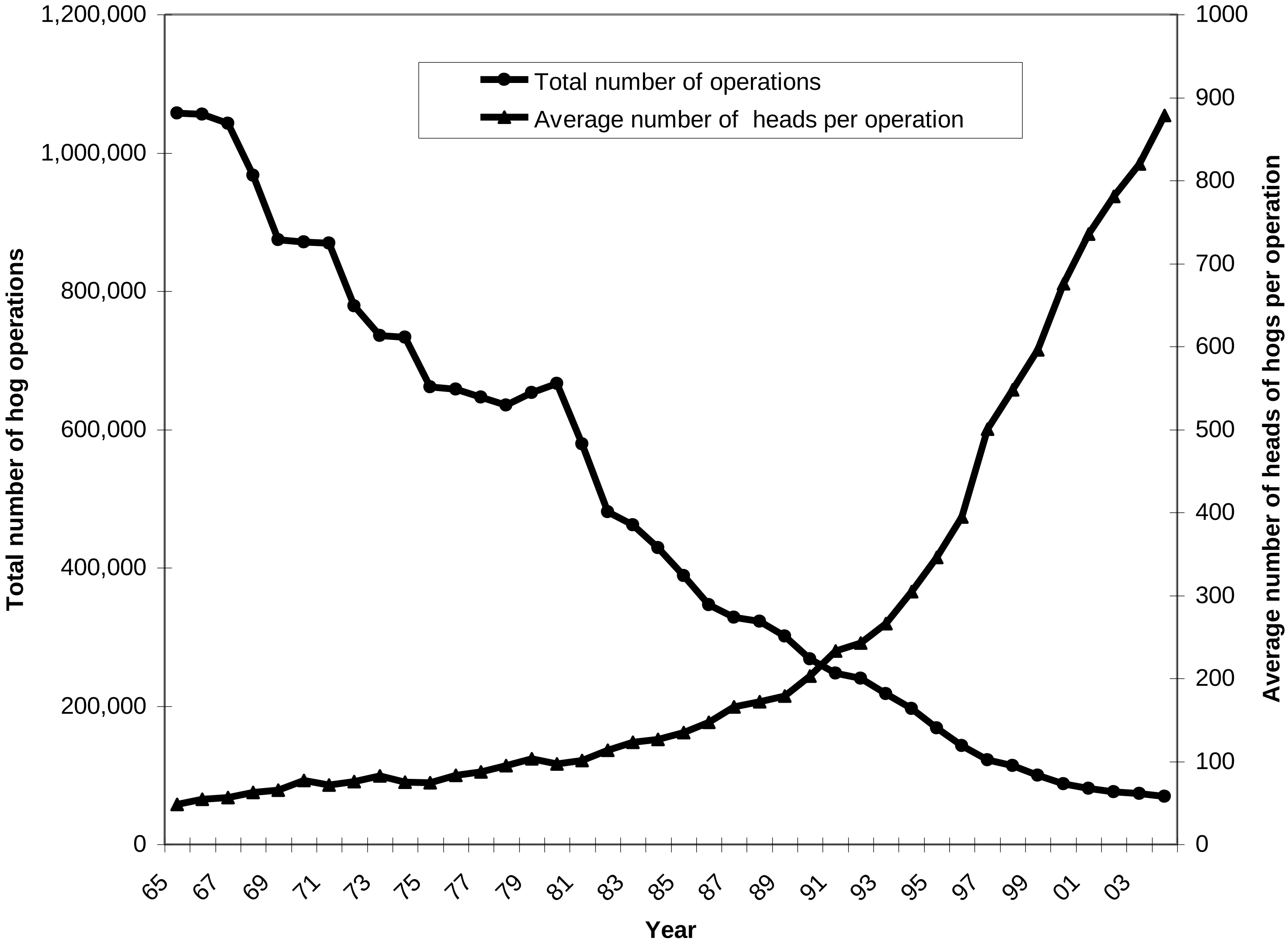
Are the Influenza A currently reservoired in animals zoonotic in nature

- Avian - Yes
- Swine - Yes
- Equine - Yes
- Canine – Not yet
- Marine mammal – Not yet

Swine Influenza

Family Farm

Swine confined animal feeding operations (CAFOs); intensive swine farming



Adapted from US Department of Agriculture, National Agricultural Statistics Service.Historical data. Available at: www.usda.gov/nass/pubs/histdata.htm.

Intensive Swine Production & SIV

- SIV is endemic where modern production facilities are common
- Risk factors for sow-herd SIV seropositivity - pigs density, an external source of breeding pigs, total animals on the site, and closeness of barns
- Risk factors for finisher-herd SIV positivity - SIV positive sows, large herd size, high pig farm density, and farrow-to-finish type of farm.

Influenza Other Respir Viruses. 2008 May;2(3):99-105
Can J Vet Res. 2008 Jan;72(1):7-17

Pigs may often be involved in novel influenza virus generation

Zoonoses and Public Health

REVIEW ARTICLE

The Role of Swine in the Generation of Novel Influenza Viruses

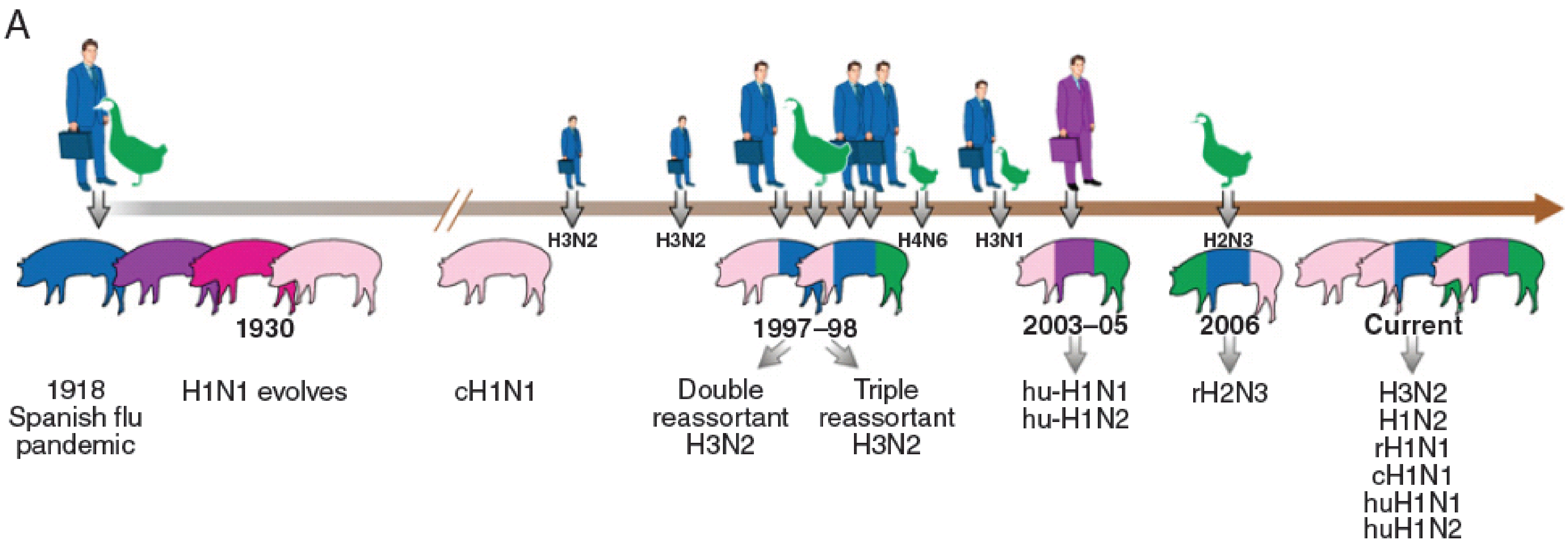
W. Ma[1], K. M. Lager[2], A. L. Vincent[2], B. H. Janke[3], M. R. Gramer[4] and J. A. Richt[1,2]

[1] Department of Diagnostic Medicine/Pathobiology, College of Veterinary Medicine, Kansas State University, Manhattan, KS, USA
[2] Virus and Prion Diseases of Livestock Research Unit, National Animal Disease Center, Ames, IA, USA
[3] Department of Veterinary Diagnostic and Production Animal Medicine, College of Veterinary Medicine, Iowa State University, Ames, IA, USA
[4] University of Minnesota Veterinary Diagnostic Laboratory, College of Veterinary Medicine, St. Paul, MN, USA

Impacts

- Swine can be a mixing vessel for human, avian and swine influenza A viruses.
- This mixing can lead to unique reassortant influenza A viruses being generated in swine.
- The unique viruses may infect humans.

Zoonoses Public Health. **56** (2009) 326–337



Amy L. Vincent, Wenjun Ma, Kelly M. Lager, Bruce H. Janke, and Jürgen A. Richt, Swine Influenza Viruses: A North American Perspective. In Karl Maramorosch, Aaron J. Shatkin, and Frederick A. Murphy, editors: Advances in Virus Research, Vol. 72, Burlington: Academic Press, 2008, pp.127-154.

Studies of Swine-exposed Persons for Swine Influenza Infections

- Myers KP, Olsen CW, Setterquist SF, Capuano AW, Donham KJ, Thacker EL, Merchant JA, Gray GC. Are Swine Workers in the United States at Increased Risk of Infection with Zoonotic Influenza Virus?.Clin Infect Dis 2006:42:14-20. PMC1673212.
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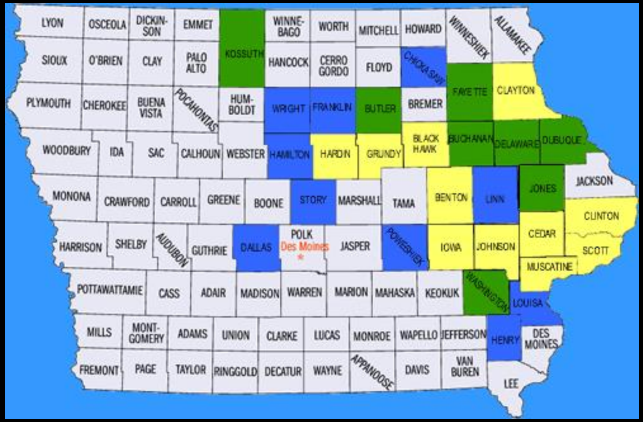
Population-based Surveillance for Zoonotic Influenza A (NIAID R21)

- **Design – 2-year prospective, controlled study of farmers who were occupationally exposed to swine or poultry (n=805); 29 counties in Iowa**
- **Exposure questionnaires – at enrollment, 12-months, and 24 months**
- **Specimen collection – Sera collection upon enrollment, at 12 months and 24 months; viral specimens and questionnaire when ill**



- Gray GC, McCarthy T, Capuano AW, Setterquist SF, Olsen CF, Alavanja MC, Lynch CF. Swine Workers and Swine Influenza Virus Infections. Emerg Infect Dis 2007;13:1871-78

Table 3. Enrollment - analyses of risk factors using proportional odds model, university controls as reference.

		Swine H1N1	Swine H1N2
		Adjusted OR (95% CI)	**Adjusted OR (95% CI)**
Swine exposure			
AHS - worked in swine production	**707**	**54.9 (13.0-232.6)**	**13.5 (6.1-29.7)**
AHS - Never worked in swine production	**80**	**28.2 (6.1-130.1)**	**6.9 (2.8-17.2)**
Non AHS - Controls	**79**	reference	reference
Age continuous	**866**	**0.97(0.96-0.98)**	---
Gender			
Male	**484**	**3.3(2.4-4.5)**	**3(2.2-4)**
Female	**382**	reference	reference
Received flu shot in the past 4 years			
Yes	**479**	**1.4(1.1-1.9)**	---
No/Unsure	**387**	reference	---
Human H1N1			
Positive	**347**	---	1.8(1.4-2.4)
Negative	**519**	---	reference

- Gray GC, McCarthy T, Capuano AW, Setterquist SF, Olsen CF, Alavanja MC, Lynch CF. Swine Workers and Swine Influenza Virus Infections. Emerg Infect Dis 2007;13:1871-78

VECTOR-BORNE AND ZOONOTIC DISEASES
Volume 6, Number 4, 2006

Research Paper

Confined Animal Feeding Operations as Amplifiers of Influenza

ROBERTO A. SAENZ,[1] HERBERT W. HETHCOTE,[2] and GREGORY C. GRAY[3]

ABSTRACT

Influenza pandemics occur when a novel influenza strain, often of animal origin, becomes transmissible between humans. Domestic animal species such as poultry or swine in confined animal feeding operations (CAFOs) could serve as local amplifiers for such a new strain of influenza. A mathematical model is used to examine the transmission dynamics of a new influenza virus among three sequentially linked populations: the CAFO species, the CAFO workers (the bridging population), and the rest of the local human population. Using parameters based on swine data, simulations showed that when CAFO workers comprised 15–45% of the community, human influenza cases increased by 42–86%. Successful vaccination of at least 50% of CAFO workers cancelled the amplification. A human influenza epidemic due to a new virus could be locally amplified by the presence of confined animal feeding operations in the community. Thus vaccination of CAFO workers would be an effective use of a pandemic vaccine. Key Words: Influenza in birds—Influenza A virus—Swine—Zoonoses—Communicable diseases—Models—Theoretical. Vector-Borne Zoonotic Dis. 6, 338–346.

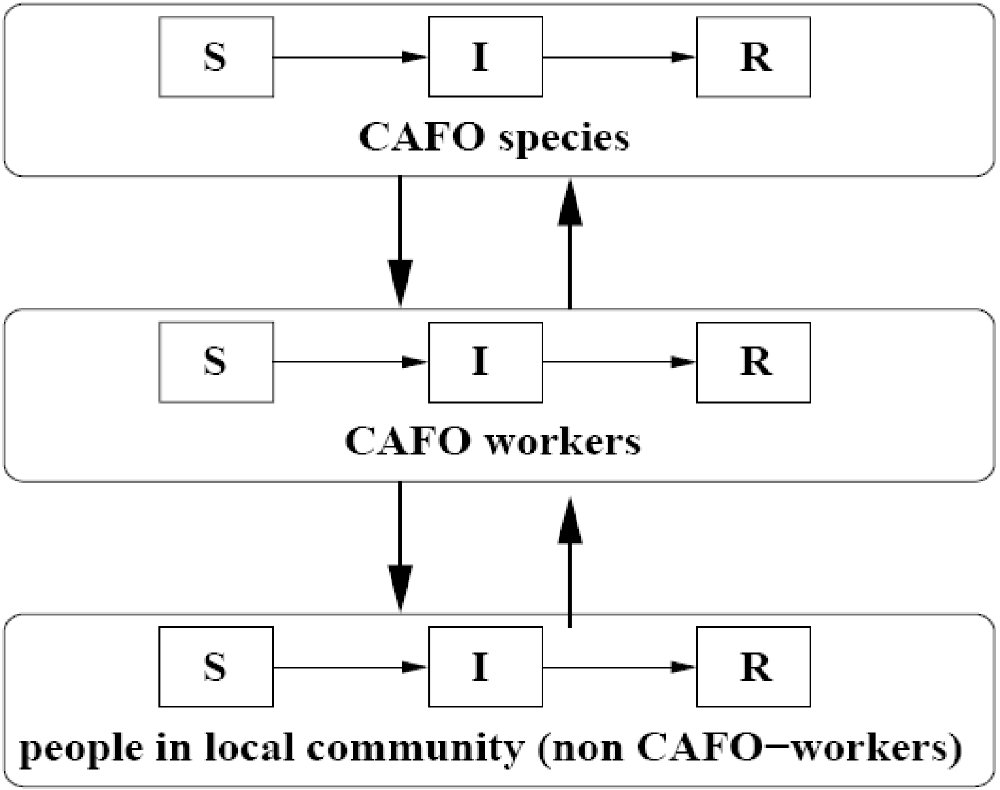


Figure 1. Transmission dynamics between the CAFO species, CAFO workers, and the rest of the local community. In each group susceptibles (S) become infected (I) and then removed (R) after recovery.

Saenz RA, Hethcote HW, Gray GC. Confined animal feeding operations as amplifiers of influenza. Vector Borne Zoonotic Dis, 2006;6:338-46 .

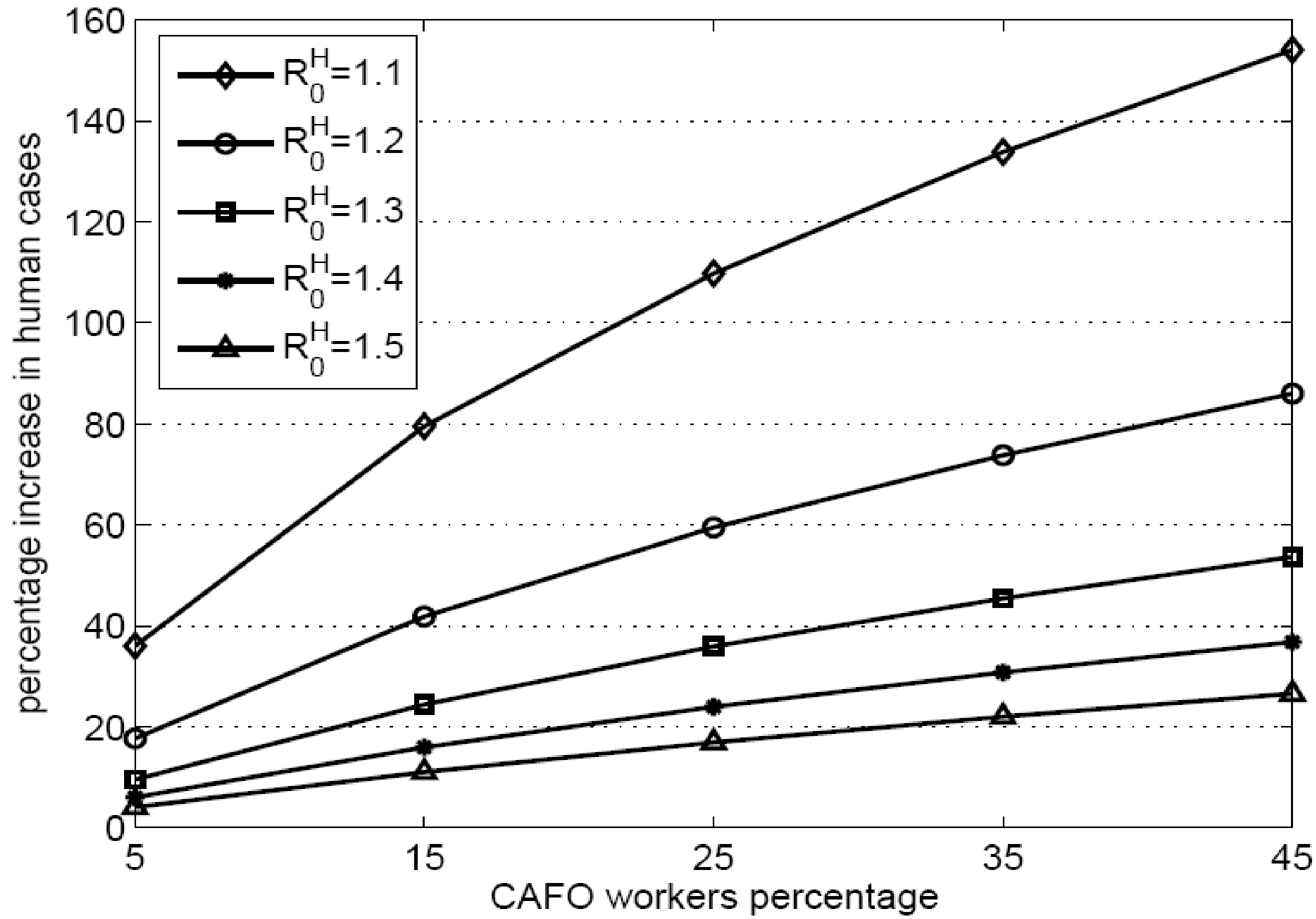


Figure 5. Percentage increases in the final size of the epidemic as a function of the percentage of CAFO workers in the community with R_0^H=1.1, 1.2, 1.3, 1.4, and 1.5. CAFO workers are 5%, 15%, 25%, 35%, and 45% of the local population.

Saenz RA, Hethcote HW, Gray GC. Confined animal feeding operations as amplifiers of influenza. Vector Borne Zoonotic Dis, 2006;6:338-46 .

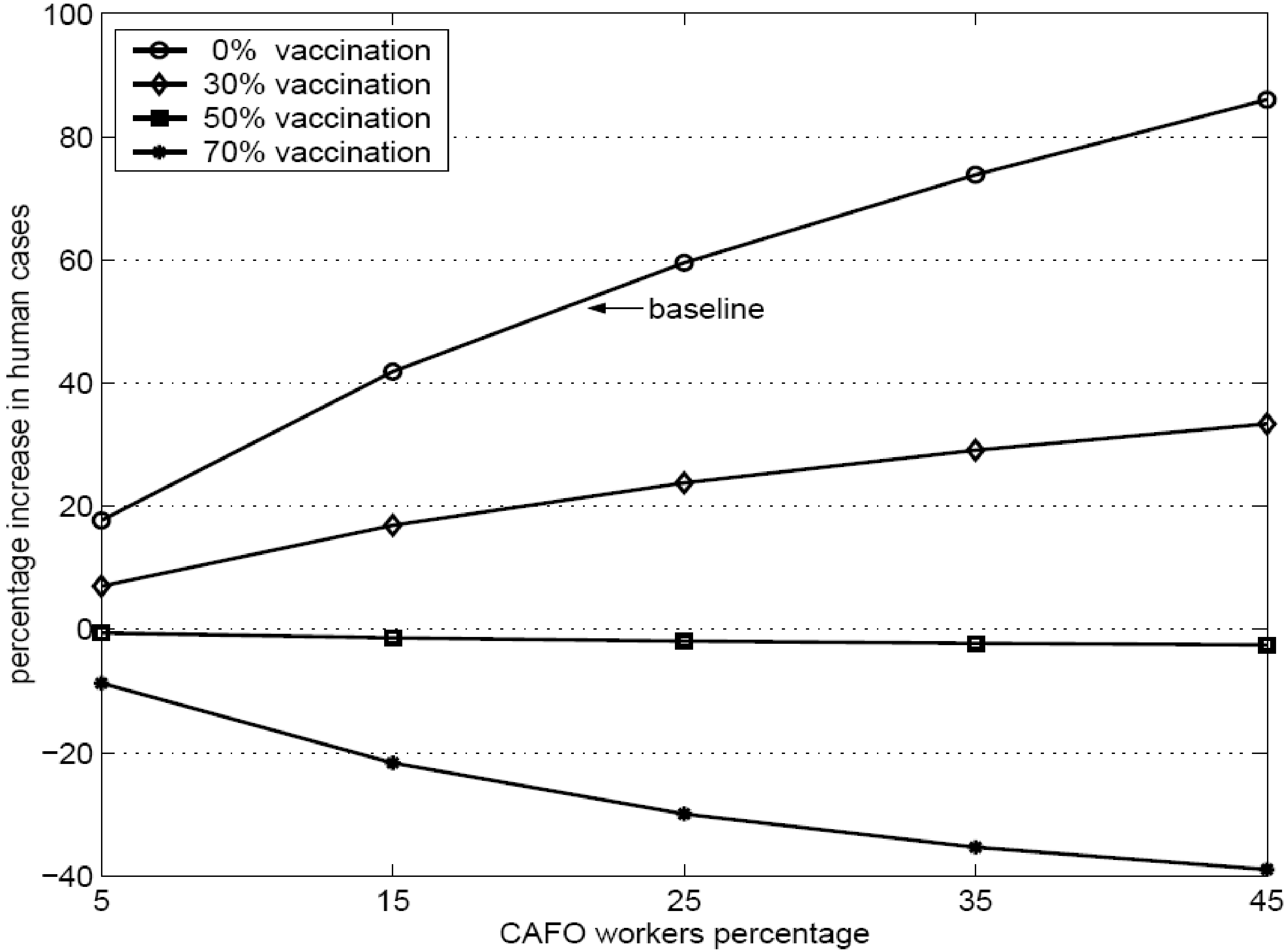


Figure 4. Percentage increases in the final size of the human influenza epidemic as a function of the percentage of CAFO workers in the community. The curves correspond to pre-epidemic successful vaccination of 0% to 70% of the CAFO workers. Local communities with 5%, 15%, 25%, 35%, and 45% of CAFO workers are considered.

Saenz RA, Hethcote HW, Gray GC. Confined animal feeding operations as amplifiers of influenza. Vector Borne Zoonotic Dis, 2006;6:338-46.

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Pandemic influenza planning: Shouldn't swine and poultry workers be included?

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PERSPECTIVES

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COMMENTARIES

The Importance of Including Swine and Poultry Workers in Influenza Vaccination Programs

GC Gray[1] and WS Baker[1]

Sensing the threat of an influenza pandemic, many countries are developing influenza pandemic prevention and control strategies. Such plans often focus efforts on detecting outbreaks and protecting leaders, health-care workers, and outbreak responders. Considering recent research, we argue that prevention plans should also include swine and poultry workers. Ignoring these workers could result in an increased probability of generating novel viruses, as well as the acceleration of a pandemic's morbidity and mortality.

Zoonotic influenza A infections among swine and poultry workers

The key risk factors for human infections with swine or avian influenza virus is exposure to diseased pigs or birds.[2] Recent US epidemiological studies suggest that agricultural workers, including veterinarians, are at increased risk of zoonotic influenza virus infection. A 2002 study reported that modern swine workers were considerably more likely to have antibodies against new swine viruses, in comparison with controls not exposed to swine.[3] A recent study found that swine farmers, swine veterinarians, and pork-processing workers were significantly more likely to have elevated antibodies against swine H1N1 and H1N2 viruses, which could not be attributed to exposure to human H1 influenza virus or vaccines.[4] This same study showed that the adjusted

Facing pandemic influenza threats: The importance of including poultry and swine workers in preparedness plans[1]

G. C. Gray[2] and G. Kayali

Center for Emerging Infectious Diseases, Department of Epidemiology, College of Public Health, University of Iowa, Iowa City 52242

ABSTRACT Recent research has shown that poultry and swine workers, especially those with intense exposures, are at increased risk of zoonotic influenza virus infections. In multiple studies, US poultry workers and poultry veterinarians have evidence of previous infections with avian influenza virus. Similarly, US swine workers have strong evidence of previous and acute infections with swine influenza viruses. Mathematical modeling has demonstrated that such workers may accelerate the spread of pandemic viruses in their rural communities. Because these workers may contribute to the novel generation of viruses and serve as a bridging population in the cross-species sharing of influenza viruses, it seems prudent to include poultry and swine workers in influenza preparedness programs. Possible preventive and control interventions include special education programs to increase workers' use of personal protective equipment such as gloves, increased surveillance for influenza viruses among workers and their animals, recommendations that workers seek medical attention should they develop influenza-like illness, and workers' priority receipt of annual and pandemic influenza vaccines.

Key words: influenza, zoonosis, occupational exposure, communicable disease, emerging

2009 Poultry Science 88:880–884
doi:10.3382/ps.2008-00335

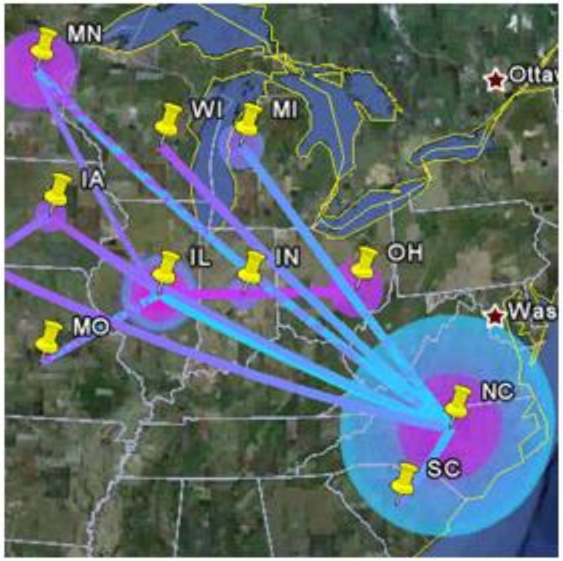
Are Pigs Bringing the Flu to Your State? Researchers Map Influenza Spread by Hogs [Animation]

New animations show how various strains of the flu travel across the U.S. to mingle in the major hog production centers in the Midwest, suggesting strategies to monitor for future pandemics

By Katherine Harmon

MALTA—For millions of U.S. pigs, their short lives are going to be full of travel. Born in one state, fattened and slaughtered in another, these hogs get around. And so, too, do their infections.

As carriers—and fertile mixing grounds—for influenza A strains that could cause illness or even pandemic in humans, hogs are important subjects for flu researchers. But with such a massive industry across the U.S., scientists are only just starting to get a handle on this continual mingling of various stocks of hogs and viruses, Martha Nelson, a researcher at the Fogarty International Center at the National Institutes of Health,



A PATTERN TO PREDICT PANDEMICS? Swine are being shipped all over the U.S., carrying with them a variety of different flu strains.
Image: Nelson/Lemey/Tan/Vincent/Lam

Nelson Plos Pathogens 2001;7 e1002077

Spatial Dynamics of Human-Origin H1 Influenza A Virus in North American Swine

Martha I. Nelson[1*], Philippe Lemey[2], Yi Tan[1], Amy Vincent[3], Tommy Tsan-Yuk Lam[4], Susan Detmer[5], Cécile Viboud[1], Marc A. Suchard[6], Andrew Rambaut[1,7], Edward C. Holmes[1,4], Marie Gramer[5]

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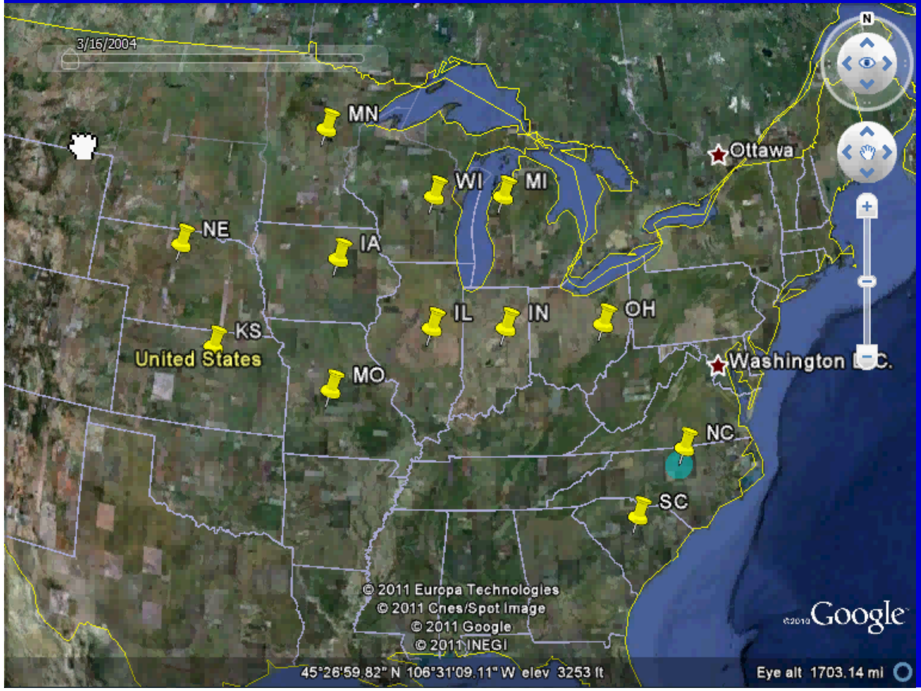
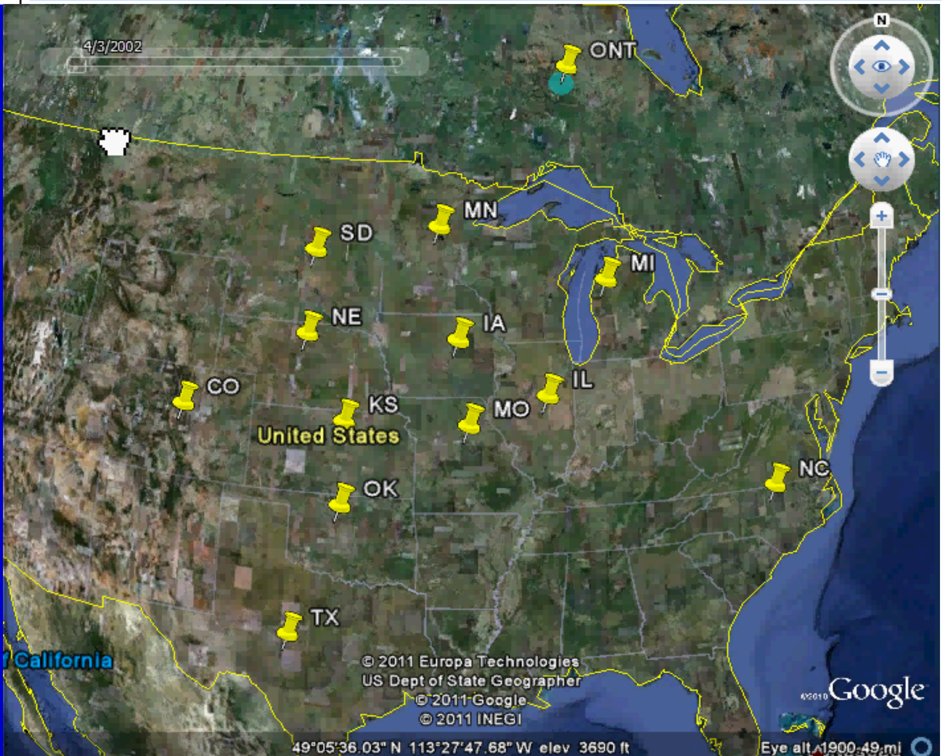
Abstract

The emergence and rapid global spread of the swine-origin H1N1/09 pandemic influenza A virus in humans underscores the importance of swine populations as reservoirs for genetically diverse influenza viruses with the potential to infect humans. However, despite their significance for animal and human health, relatively little is known about the phylogeography of swine influenza viruses in the United States. This study utilizes an expansive data set of hemagglutinin (HA1) sequences (n = 1516) from swine influenza viruses collected in North America during the period 2003–2010. With these data we investigate the spatial dissemination of a novel influenza virus of the H1 subtype that was introduced into the North American swine population via two separate human-to-swine transmission events around 2003. Bayesian phylogeographic analysis reveals that the spatial dissemination of this influenza virus in the US swine population follows long-distance swine movements from the Southern US to the Midwest, a corn-rich commercial center that imports millions of swine annually. Hence, multiple genetically diverse influenza viruses are introduced and co-circulate in the Midwest, providing the opportunity for genomic reassortment. Overall, the Midwest serves primarily as an ecological sink for swine influenza in the US, with sources of virus genetic diversity instead located in the Southeast (mainly North Carolina) and South-central (mainly Oklahoma) regions. Understanding the importance of long-distance pig transportation in the evolution and spatial dissemination of the influenza virus in swine may inform future strategies for the surveillance and control of influenza, and perhaps other swine pathogens.





Introductions and Evolution of Human-Origin Seasonal Influenza A Viruses in Multinational Swine Populations

Martha I. Nelson,[a] David E. Wentworth,[b] Marie R. Culhane,[c] Amy L. Vincent,[d] Cecile Viboud,[a] Matthew P. LaPointe,[b] Xudong Lin,[b] Edward C. Holmes,[e] Susan E. Detmer[f]

Fogarty International Center, National Institutes of Health, Bethesda, Maryland, USA[a]; J. Craig Venter Institute, Rockville, Maryland, USA[b]; University of Minnesota Veterinary Diagnostic Laboratory, St. Paul, Minnesota, USA[c]; Virus and Prion Research Unit, National Animal Disease Center, USDA-ARS, Ames, Iowa, USA[d]; Marie Bashir Institute for Infectious Diseases and Biosecurity, Charles Perkins Centre, School of Biological Sciences and Sydney Medical School, University of Sydney, NSW, Australia[e]; Western College of Veterinary Medicine, University of Saskatchewan, Saskatchewan, Canada[f]

ABSTRACT

The capacity of influenza A viruses to cross species barriers presents a continual threat to human and animal health. Knowledge of the human-swine interface is particularly important for understanding how viruses with pandemic potential evolve in swine hosts. We sequenced the genomes of 141 influenza viruses collected from North American swine during 2002 to 2011 and identified a swine virus that possessed all eight genome segments of human seasonal A/H3N2 virus origin. A molecular clock analysis indicates that this virus—A/sw/Saskatchewan/02903/2009(H3N2)—has likely circulated undetected in swine for at least 7 years. For historical context, we performed a comprehensive phylogenetic analysis of an additional 1,404 whole-genome sequences from swine influenza A viruses collected globally during 1931 to 2013. Human-to-swine transmission occurred frequently over this time period, with 20 discrete introductions of human seasonal influenza A viruses showing sustained onward transmission in swine for at least 1 year since 1965. Notably, human-origin hemagglutinin (H1 and H3) and neuraminidase (particularly N2) segments were detected in swine at a much higher rate than the six internal gene segments, suggesting an association between the acquisition of swine-origin internal genes via reassortment and the adaptation of human influenza viruses to new swine hosts. Further understanding of the fitness constraints on the adaptation of human viruses to swine, and vice versa, at a genomic level is central to understanding the complex multihost ecology of influenza and the disease threats that swine and humans pose to each other.

IMPORTANCE

The swine origin of the 2009 A/H1N1 pandemic virus underscored the importance of understanding how influenza A virus evolves in these animals hosts. While the importance of reassortment in generating genetically diverse influenza viruses in swine is well documented, the role of human-to-swine transmission has not been as intensively studied. Through a large-scale sequencing effort, we identified a novel influenza virus of wholly human origin that has been circulating undetected in swine for at least 7 years. In addition, we demonstrate that human-to-swine transmission has occurred frequently on a global scale over the past decades but that there is little persistence of human virus internal gene segments in swine.

Human influenza viruses may be introduced into modern swine farms

Swine Outbreak of Pandemic Influenza A Virus on a Canadian Research Farm Supports Human-to-Swine Transmission

Sarah E. Forgie,[1,a] Julia Keenliside,[2,3,a] Craig Wilkinson,[1] Richard Webby,[7] Patricia Lu,[2] Ole Sorensen,[2] Kevin Fonseca,[4] Subrata Barman,[7] Adam Rubrum,[7] Evelyn Stigger,[7] Thomas J. Marrie,[5] Frank Marshall,[3] Donald W. Spady,[1] Jia Hu,[1] Mark Loeb,[6] Margaret L. Russell,[3] and Lorne A. Babiuk[1]

[1]University of Alberta, Edmonton, Alberta, and [2]Alberta Agriculture and Rural Development, Edmonton, Alberta, and [3]University of Calgary, Calgary, Alberta, and [4]Provincial Laboratory for Public Health, Calgary, Alberta, and [5]Dalhousie University, Halifax, Nova Scotia, and [6]McMaster University, Hamilton, Ontario, and [7]St Jude Children's Research Hospital, Memphis, Tennessee

(See the editorial commentary by Gray et al. on pages 19–22).

Background. Swine outbreaks of pandemic influenza A (pH1N1) suggest human introduction of the virus into herds. This study investigates a pH1N1 outbreak occurring on a swine research farm with 37 humans and 1300 swine in Alberta, Canada, from 12 June through 4 July 2009.

Methods. The staff was surveyed about symptoms, vaccinations, and livestock exposures. Clinical findings were recorded, and viral testing and molecular characterization of isolates from humans and swine were performed. Human serological testing and performance of the human influenza-like illness (ILI) case definition were also studied.

Results. Humans were infected before swine. Seven of 37 humans developed ILI, and 2 (including the index case) were positive for pH1N1 by reverse-transcriptase polymerase chain reaction (RT-PCR). Swine were positive for pH1N1 by RT-PCR 6 days after contact with the human index case and developed symptoms within 24 h of their positive viral test results. Molecular characterization of the entire viral genomes from both species showed minor nucleotide heterogeneity, with 1 amino acid change each in the hemagglutinin and nucleoprotein genes. Sixty-seven percent of humans with positive serological test results and 94% of swine with positive swab specimens had few or no symptoms. Compared with serological testing, the human ILI case definition had a specificity of 100% and sensitivity of 33.3%. The only factor associated with seropositivity was working in the swine nursery.

Conclusions. Epidemiologic data support human-to-swine transmission, and molecular characterization confirms that virtually identical viruses infected humans and swine in this outbreak. Both species had mild illness and recovered without sequelae.

CID 2011:52 (1 January) • Forgie et al.

Human influenza viruses may be introduced into modern swine farms

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Introductions and Evolution of Human-Origin Seasonal Influenza A Viruses in Multinational Swine Populations

Martha I. Nelson,[a] David E. Wentworth,[b] Marie R. Culhane,[c] Amy L. Vincent,[d] Cecile Viboud,[a] Matthew P. LaPointe,[b] Xudong Lin,[b] Edward C. Holmes,[e] Susan E. Detmer[f]

Fogarty International Center, National Institutes of Health, Bethesda, Maryland, USA[a]; J. Craig Venter Institute, Rockville, Maryland, USA[b]; University of Minnesota Veterinary Diagnostic Laboratory, St. Paul, Minnesota, USA[c]; Virus and Prion Research Unit, National Animal Disease Center, USDA-ARS, Ames, Iowa, USA[d]; Marie Bashir Institute for Infectious Diseases and Biosecurity, Charles Perkins Centre, School of Biological Sciences and Sydney Medical School, University of Sydney, NSW, Australia[e]; Western College of Veterinary Medicine, University of Saskatchewan, Saskatchewan, Canada[f]

ABSTRACT

The capacity of influenza A viruses to cross species barriers presents a continual threat to human and animal health. Knowledge of the human-swine interface is particularly important for understanding how viruses with pandemic potential evolve in swine hosts. We sequenced the genomes of 141 influenza viruses collected from North American swine during 2002 to 2011 and identified a swine virus that possessed all eight genome segments of human seasonal A/H3N2 virus origin. A molecular clock analysis indicates that this virus—A/sw/Saskatchewan/02903/2009(H3N2)—has likely circulated undetected in swine for at least 7 years. For historical context, we performed a comprehensive phylogenetic analysis of an additional 1,404 whole-genome sequences from swine influenza A viruses collected globally during 1931 to 2013. Human-to-swine transmission occurred frequently over this time period, with 20 discrete introductions of human seasonal influenza A viruses showing sustained onward transmission in swine for at least 1 year since 1965. Notably, human-origin hemagglutinin (H1 and H3) and neuraminidase (particularly N2) segments were detected in swine at a much higher rate than the six internal gene segments, suggesting an association between the acquisition of swine-origin internal genes via reassortment and the adaptation of human influenza viruses to new swine hosts. Further understanding of the fitness constraints on the adaptation of human viruses to swine, and vice versa, at a genomic level is central to understanding the complex multihost ecology of influenza and the disease threats that swine and humans pose to each other.

Reports of reverse zoonoses are increasing and 43% are in livestock

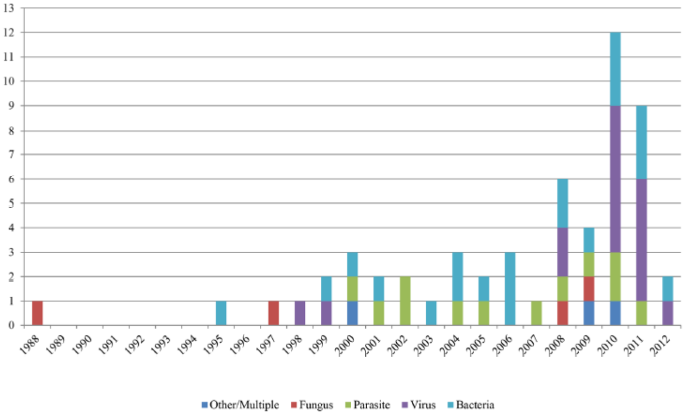

Figure 2. Timeline and frequency of reverse zoonoses publications included in this review shown by pathogen type.
doi:10.1371/journal.pone.0089055.g002

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Reverse Zoonotic Disease Transmission (Zooanthroponosis): A Systematic Review of Seldom-Documented Human Biological Threats to Animals

Ali M. Messenger[1,2], Amber N. Barnes[1], Gregory C. Gray[1,2]*

1 College of Public Health and Health Professions, University of Florida, Gainesville, Florida, United States of America, 2 Emerging Pathogens Institute, University of Florida, Gainesville, Florida, United States of America

Abstract

Background: Research regarding zoonotic diseases often focuses on infectious diseases animals have given to humans. However, an increasing number of reports indicate that humans are transmitting pathogens to animals. Recent examples include methicillin-resistant *Staphylococcus aureus*, influenza A virus, *Cryptosporidium parvum*, and *Ascaris lumbricoides*. The aim of this review was to provide an overview of published literature regarding reverse zoonoses and highlight the need for future work in this area.

Methods: An initial broad literature review yielded 4763 titles, of which 4704 were excluded as not meeting inclusion criteria. After careful screening, 56 articles (from 56 countries over three decades) with documented human-to-animal disease transmission were included in this report.

Findings: In these publications, 21 (38%) pathogens studied were bacterial, 16 (29%) were viral, 12 (21%) were parasitic, and 7 (13%) were fungal, other, or involved multiple pathogens. Effected animals included wildlife (n = 28, 50%), livestock (n = 24, 43%), companion animals (n = 13, 23%), and various other animals or animals not explicitly mentioned (n = 2, 4%). Published reports of reverse zoonoses transmission occurred in every continent except Antarctica therefore indicating a worldwide disease threat.

Interpretation: As we see a global increase in industrial animal production, the rapid movement of humans and animals, and the habitats of humans and wild animals intertwining with great complexity, the future promises more opportunities for humans to cause reverse zoonoses. Scientific research must be conducted in this area to provide a richer understanding of emerging and reemerging disease threats. As a result, multidisciplinary approaches such as One Health will be needed to mitigate these problems.


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Influenza A(H1N1)pdm09 Virus among Healthy Show Pigs, United States

Gregory C. Gray, Jeffrey B. Bender, Carolyn B. Bridges, Russell F. Daly, Whitney S. Krueger, Michael J. Male, Gary L. Heil, John A. Friary, Robin B. Derby, and Nancy J. Cox

Within 5 months after the earliest detection of human influenza A(H1N1)pdm09 virus, we found molecular and culture evidence of the virus in healthy US show pigs. The mixing of humans and pigs at swine shows possibly could further the geographic and cross-species spread of influenza A viruses.

pH1N1 in pigs by country

Generated from OIE data available from World Animal Health Information Database & sequences deposited in GenBank, August 2010…Courtesy of Dr. Amy Vincent of National Animal Disease Center, Ames, IA

Reassorted pandemic (H1N1) 2009 influenza A virus discovered from pigs in Germany

Elke Starick,[1] Elke Lange,[1] Sasan Fereidouni,[1] Claudia Bunzenthal,[2] Robert Höveler,[2] Annette Kuczka,[2] Elisabeth grosse Beilage,[3] Hans-Peter Hamann,[4] Irene Klingelhöfer,[5] Dirk Steinhauer,[5] Thomas Vahlenkamp,[1] Martin Beer[1] and Timm Harder[1]

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[4]Landesbetrieb Hessisches Landeslabor, Gießen, Germany

[5]Landesuntersuchungsamt Rheinland Pfalz, Koblenz, Germany

Reassortment of Pandemic H1N1/2009 Influenza A Virus in Swine

D. Vijaykrishna,[1,2]*† L. L. M. Poon,[1]* H. C. Zhu,[1,2] S. K. Ma,[1] O. T. W. Li,[1] C. L. Cheung,[1] G. J. D. Smith,[1,2]† J. S. M. Peiris,[1]‡ Y. Guan[1,2]‡

SCIENCE VOL 328 18 JUNE 2010

Novel H1N2 swine influenza reassortant strain in pigs derived from the pandemic H1N1/2009 virus

Ana Moreno[a,*], Livia Di Trani[b], Silvia Faccini[a], Gabriele Vaccari[b], Daniele Nigrelli[a], M. Beatrice Boniotti[a], Emiliana Falcone[b], Arianna Boni[b], Chiara Chiapponi[a], Enrica Sozzi[a], Paolo Cordioli[a]

[a]*Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna (IZSLER), Via Bianchi, 9, 25124 Brescia, Italy*
[b]*Department of Veterinary Public Health and Food Safety, Istituto Superiore di Sanità, V.le Regina Elena, 299, 0016 Rome, Italy*

Veterinary Microbiology 149 (2011) 472–477

Multiple Reassortment between Pandemic (H1N1) 2009 and Endemic Influenza Viruses in Pigs, United States

Mariette F. Ducatez, Ben Hause, Evelyn Stigger-Rosser, Daniel Darnell, Cesar Corzo, Kevin Juleen, Randy Simonson, Christy Brockwell-Staats, Adam Rubrum, David Wang, Ashley Webb, Jeri-Carol Crumpton, James Lowe, Marie Gramer, and Richard J. Webby

Emerging Infectious Diseases • www.cdc.gov/eid • Vol. 17, No. 9, September 2011

Influenza (Flu)

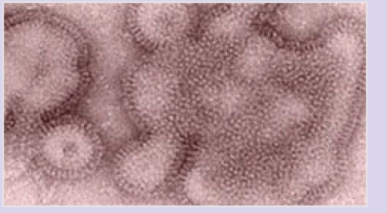
Influenza A (H3N2) Variant Virus

Language: English

Influenza viruses that normally circulate in pigs are called "variant" viruses when they are found in people. Influenza A H3N2 variant viruses (also known as "H3N2v" viruses) with the matrix (M) gene from the 2009 H1N1 pandemic virus were first detected in people in July 2011. The viruses were first identified in U.S. pigs in 2010. Infections with H3N2v have mostly been associated with prolonged exposure to pigs at agricultural fairs. Limited human-to-human spread of this virus has been detected in the past as well but no sustained or community spread of H3N2v has been identified at this time. It's possible that sporadic infections and even localized outbreaks among people with this virus will continue to occur. The Centers for Disease Control and Prevention (CDC) continues to monitor this situation closely and will report cases of H3N2v and other variant influenza viruses weekly in FluView and on the case count tables on this website.

See Past Updates »

- Background
- Basics
- Prevention
- Treatment
- News & Highlights
- **New!** Glossary of Influenza (Flu) Terms
- CDC Assessment
- Health Care Providers
- Guidance for Public Health
- Other Guidance
- Materials & Resources



Outbreak Characterization

- Localized outbreaks
- Swine-to-human transmission; rare, limited human-to-human
- No sustained or community transmission

Case Count Table »

Info for Specific Audiences

- People Who Raise Pigs
- Fair Managers and Exhibitors

Since Aug 2011,345 human cases in 13 states as of Oct 2015

Pigs may have no signs of infection and still carry & aerosolize novel influenza

Transbound Emerg Dis. 2014 Feb;61(1):28-36. doi: 10.1111/j.1865-1682.2012.01367.x. Epub 2012 Jul 25.

Detection of airborne influenza a virus in experimentally infected pigs with maternally derived antibodies.

Corzo CA[1], Allerson M, Gramer M, Morrison RB, Torremorell M.

Subclinical Influenza Virus A Infections in Pigs Exhibited at Agricultural Fairs, Ohio, USA, 2009–2011

Andrew S. Bowman, Jacqueline M. Nolting, Sarah W. Nelson, and Richard D. Slemons

ORIGINAL ARTICLE

Simultaneous Infection of Pigs and People with Triple-Reassortant Swine Influenza Virus H1N1 at a U.S. County Fair

M. L. Killian[1], S. L. Swenson[1], A. L. Vincent[2], J. G. Landgraf[1], B. Shu[3], S. Lindstrom[3], X. Xu[3], A. Klimov[3], Y. Zhang[4] and A. S. Bowman[5]

[1] Diagnostic Virology Laboratory, National Veterinary Services Laboratories, USDA, Animal and Plant Health Inspection Service, Ames, IA, USA
[2] Virus and Prion Diseases of Livestock Research Unit, National Animal Disease Center, USDA, Agricultural Research Service, Ames, IA, USA
[3] Virus Surveillance and Diagnostic Branch, Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA
[4] Animal Disease Diagnostic Laboratory, Reynoldsburg, OH, USA
[5] Veterinary Preventive Medicine, The Ohio State University, Columbus, OH, USA

Impacts

- Infection of humans and pigs with influenza virus was identified simultaneously at a county fair.
- Comparison of the viruses indicates they are identical, which means the virus was either transmitted from the pigs to the people or from the people to the pigs.
- Tests show the pigs had been infected or vaccinated with other strains of influenza before arriving at the fair.

Zoonoses and Public Health, 2013, **60**, 196–201

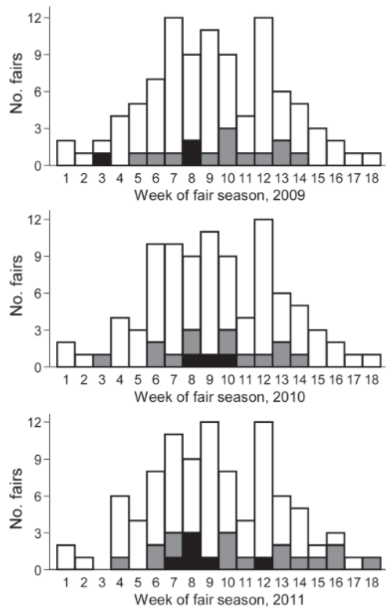


Figure. Frequency distribution of agricultural fairs, by week of the state fair season, Ohio, June–October 2009–2011. Black bar sections, fairs with pigs positive for influenza virus A; gray bar sections, fairs with no pigs positive for influenza virus A; white bar sections, fairs not enrolled in this study.

Emerging Infectious Diseases • www.cdc.gov/eid • Vol. 18, No. 12, December 2012

Ohio reports 98 human cases of H3N2v influenza

OHIO | AUGUST 26, 2012 | BY: ROBERT HERRIMAN

"We're not particularly surprised to see what looks like limited human-to-human transmission," says Dr. Bresee.
Credits: Mark Wilson/Getty Images

RELATED TOPICS

- Ohio
- H3N2v
- swine flu

The Centers for Disease Control and Prevention (CDC) **reported Friday** that with the addition of 52 new human cases of H3N2v influenza, the total number of cases seen nationwide since July is 276.

Human Infections With Influenza A(H3N2) Variant Virus in the United States, 2011–2012

Scott Epperson,[1] Michael Jhung,[1] Shawn Richards,[2] Patricia Quinlisk,[3] Lauren Ball,[4] Mària Moll,[5] Rachelle Boulton,[6] Loretta Haddy,[7] Matthew Biggerstaff,[1] Lynnette Brammer,[1] Susan Trock,[1] Erin Burns,[1] Thomas Gomez,[8] Karen K. Wong,[9] Jackie Katz,[1] Stephen Lindstrom,[1] Alexander Klimov,[1] Joseph S. Bresee,[1] Daniel B. Jernigan,[1] Nancy Cox,[1] and Lyn Finelli[1]; for the Influenza A (H3N2)v Virus Investigation Team[a]

[1]Influenza Division, National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, Atlanta, Georgia; [2]Indiana State Department of Health, Indianapolis; [3]Iowa Department of Public Health, Des Moines; [4]Maine Center for Disease Control and Prevention, Augusta; [5]Pennsylvania Department of Health, Harrisburg; [6]Utah Department of Health, Salt Lake City; [7]West Virginia Bureau for Public Health, Charleston; [8]US Department of Agriculture, Animal and Plant Health Inspection Service, Veterinary Services, and [9]Epidemic Intelligence Service assigned to the Influenza Division, Centers for Disease Control and Prevention, Atlanta, Georgia

Background. During August 2011–April 2012, 13 human infections with influenza A(H3N2) variant (H3N2v) virus were identified in the United States; 8 occurred in the prior 2 years. This virus differs from previous variant influenza viruses in that it contains the matrix (M) gene from the Influenza A(H1N1)pdm09 pandemic influenza virus.

Methods. A case was defined as a person with laboratory-confirmed H3N2v virus infection. Cases and contacts were interviewed to determine exposure to swine and other animals and to assess potential person-to-person transmission.

Results. Median age of cases was 4 years, and 12 of 13 (92%) were children. Pig exposure was identified in 7 (54%) cases. Six of 7 cases with swine exposure (86%) touched pigs, and 1 (14%) was close to pigs without known direct contact. Six cases had no swine exposure, including 2 clusters of suspected person-to-person transmission. All cases had fever; 12 (92%) had respiratory symptoms, and 3 (23%) were hospitalized for influenza. All 13 cases recovered.

Conclusions. H3N2v virus infections were identified at a high rate from August 2011 to April 2012, and cases without swine exposure were identified in influenza-like illness outbreaks, indicating that limited person-to-person transmission likely occurred. Variant influenza viruses rarely result in sustained person-to-person transmission; however, the potential for this H3N2v virus to transmit efficiently is of concern. With minimal preexisting immunity in children and the limited cross-protective effect from seasonal influenza vaccine, the majority of children are susceptible to infection with this novel influenza virus.

Keywords. influenza; surveillance; public health.

Outbreak of Variant Influenza A(H3N2) Virus in the United States

Michael A. Jhung,[1] Scott Epperson,[1] Matthew Biggerstaff,[1] Donna Allen,[8] Amanda Balish,[1] Nathelia Barnes,[1] Amanda Beaudoin,[9] LaShondra Berman,[1] Sally Bidol,[6] Lenee Blanton,[1] David Blythe,[15] Lynnette Brammer,[1] Tiffany D'Mello,[1] Richard Danila,[7] William Davis,[1] Sietske de Fijter,[12] Mary DiOrio,[12] Lizette O. Durand,[2] Shannon Emery,[1] Brian Fowler,[12] Rebecca Garten,[1] Yoran Grant,[5] Adena Greenbaum,[2] Larisa Gubareva,[1] Fiona Havers,[2] Thomas Haupt,[13] Jennifer House,[8] Sherif Ibrahim,[14] Victoria Jiang,[1] Seema Jain,[1] Daniel Jernigan,[1] James Kazmierczak,[13] Alexander Klimov,[1] Stephen Lindstrom,[1] Allison Longenberger,[10] Paul Lucas,[4] Ruth Lynfield,[7] Meredith McMorrow,[1] Maria Moll,[10] Craig Morin,[7] Stephen Ostroff,[10] Shannon L. Page,[12] Sarah Y. Park,[11] Susan Peters,[6] Celia Quinn,[3] Carrie Reed,[1] Shawn Richards,[8] Joni Scheftel,[7] Owen Simwale,[10] Bo Shu,[1] Kenneth Soyemi,[4] Jill Stauffer,[8] Craig Steffens,[1] Su Su,[1] Lauren Torso,[10] Timothy M. Uyeki,[1] Sara Vetter,[7] Julie Villanueva,[1] Karen K. Wong,[2] Michael Shaw,[1] Joseph S. Bresee,[1] Nancy Cox,[1] and Lyn Finelli[1]

[1]Influenza Division, National Center for Immunization and Respiratory Disease, and [2]Epidemic Intelligence Service assigned to the Influenza Division, Centers for Disease Control and Prevention, Atlanta, Georgia; [3]Epidemic Intelligence Service assigned to the Ohio Department of Health, Columbus; [4]Illinois Department of Public Health, Springfield; [5]Epidemic Intelligence Service assigned to the Illinois Department of Public Health, Springfield; [6]Michigan Department of Community Health, Lansing; [7]Minnesota Department of Health, St. Paul; [8]Indiana State Department of Health, Indianapolis; [9]Epidemic Intelligence Service assigned to the Pennsylvania Department of Health, Harrisburg; [10]Pennsylvania Department of Health, Harrisburg; [11]Hawaii Department of Health, Honolulu; [12]Ohio Department of Health, Columbus; [13]Wisconsin Department of Health Services, Madison; [14]West Virginia Bureau for Public Health, Charleston; and [15]Maryland Department of Health and Mental Hygiene, Baltimore

(See the Editorial Commentary by Gray and Cao on pages 1713–4.)

Background. Variant influenza virus infections are rare but may have pandemic potential if person-to-person transmission is efficient. We describe the epidemiology of a multistate outbreak of an influenza A(H3N2) variant virus (H3N2v) first identified in 2011.

Methods. We identified laboratory-confirmed cases of H3N2v and used a standard case report form to characterize illness and exposures. We considered illness to result from person-to-person H3N2v transmission if swine contact was not identified within 4 days prior to illness onset.

Results. From 9 July to 7 September 2012, we identified 306 cases of H3N2v in 10 states. The median age of all patients was 7 years. Commonly reported signs and symptoms included fever (98%), cough (85%), and fatigue (83%). Sixteen patients (5.2%) were hospitalized, and 1 fatal case was identified. The majority of those infected reported agricultural fair attendance (93%) and/or contact with swine (95%) prior to illness. We identified 15 cases of possible person-to-person transmission of H3N2v. Viruses recovered from patients were 93%–100% identical and similar to viruses recovered from previous cases of H3N2v. All H3N2v viruses examined were susceptible to oseltamivir and zanamivir and resistant to adamantane antiviral medications.

Conclusions. In a large outbreak of variant influenza, the majority of infected persons reported exposures, suggesting that swine contact at an agricultural fair was a risk for H3N2v infection. We identified limited person-to-person H3N2v virus transmission, but found no evidence of efficient or sustained person-to-person transmission. Fair managers and attendees should be aware of the risk of swine-to-human transmission of influenza viruses in these settings.

Influenza Virus Surveillance in Swine
Program Overview for Veterinarians

Passive and voluntary surveillance

US News » Iowa reports H1N1v case, 10th 'swine flu' case in Iowa since 2005

Iowa reports H1N1v case, 10th 'swine flu' case in Iowa since 2005

Posted by Robert Herriman on August 28, 2015 // 1 Comment

The Centers for Disease Control and Prevention (CDC) reported today one human infection with a novel influenza A virus from the state of Iowa. The person was infected with an influenza A (H1N1) variant (H1N1v) virus and was hospitalized as a result of their illness. No human-to-human transmission has been identified and the case reported close contact with swine in the week prior to illness onset.

Pig and piglets/Agricultural Research Services

Iowa has reported 10 "variant viruses" (H1N1v-4 and H3N2v-6) since 2005.

When an influenza virus that normally circulates in swine is detected in a person, it is called a variant influenza virus and is labeled with a 'v'.

Influenza viruses such as H1N1(v) and other related variants are not unusual in swine and can be directly transmitted from swine to people and from people to swine.

When humans are in close proximity to live swine, such as in barns and livestock exhibits at fairs, movement of these viruses can occur back and forth between humans and animals.

Benefits of modern agriculture production

- Reduction in pig diseases
- Food safety
- Animal well-being
- Lower costs

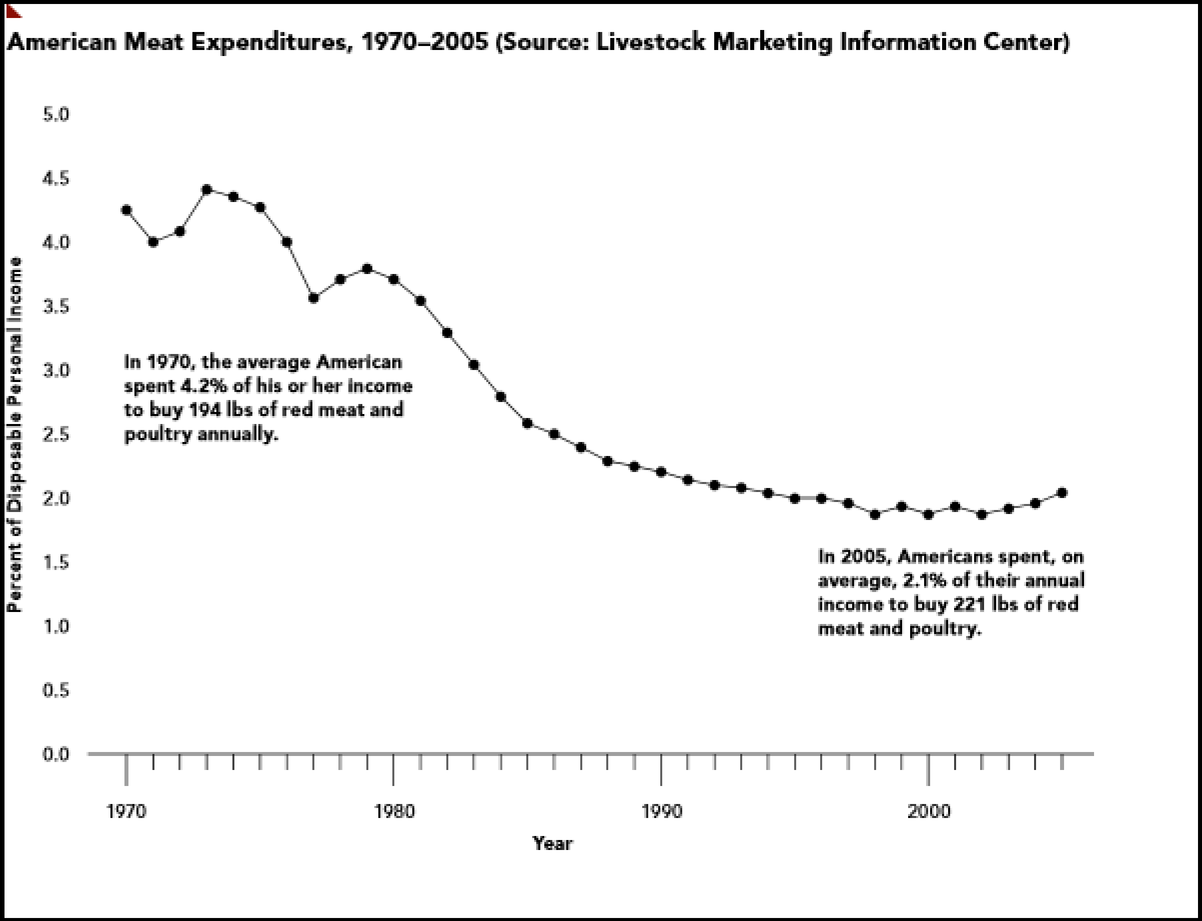
Modern Pig Farming has Reduced Many Severe or Overt Pig Diseases

- ✓ Physical barriers
- ✓ Rodent control
- ✓ Fly control
- ✓ Safe feed
- ✓ Safe water
- ✓ Isolate pigs from wild animals, stray domestic animals
- ✓ Vehicle control
- ✓ Visitor control

- Led to elimination of a number of "foreign animal diseases" in US pigs. Example include swine fevers and foot-and-mouth disease.
- Has reduced many swine zoonoses: brucellosis, trichinosis, leptospirosis, and cysticercosis.
- Has controlled the spread of epidemic disease causing reduced growth and mortality in pigs: erysipelas, pseudorabies, and swine pox

Modern Production Lowers Pork Costs

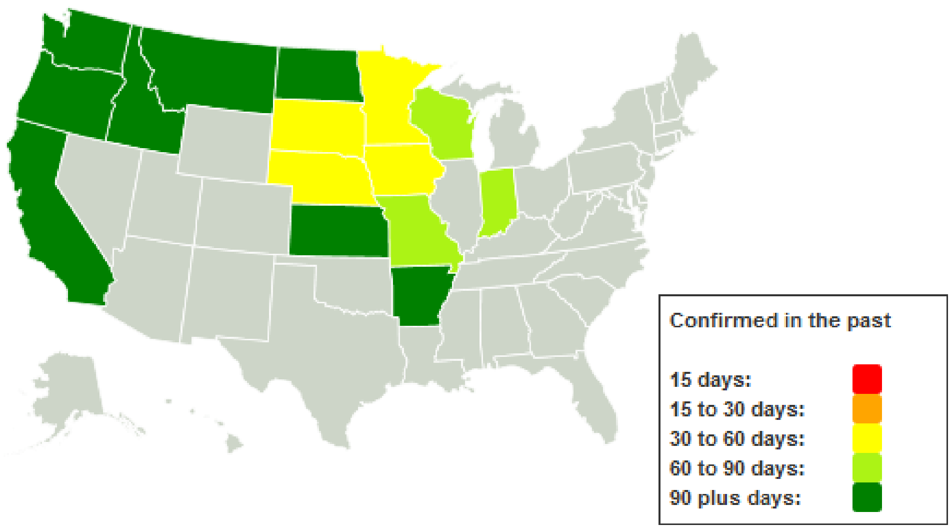
- Fewer workers
- Fewer pig losses
- More efficient use of feed
- Faster pig growth



Perhaps US Animal Production Biosecurity is Not as Good As We Once Thought

ALL Findings

Update on Avian Influenza Findings
Poultry Findings Confirmed by USDA's National Veterinary Services Laboratories



223 Detections Reported	**48,091,293** Birds Affected
12/19/14 First Detection Reported	**6/17/15** Last Detection Reported

Swine Influenza

The message seems clear that swine influenza viruses (SIV)

- Frequently infect persons exposed to pigs
- Swine shows may accelerate transmission among both pigs and man
- Can be transmitted from humans-to-humans
- SIV may cause severe human disease
- You cannot understand this problem by waiting for human cases of SIV to enter your hospital and studying the virus type
- The only way forward is a One Health research approach

Clinical Infectious Diseases Advance Access published October 24, 2013

EDITORIAL COMMENTARY

Variant Influenza A(H3N2) Virus: Looking Through a Glass, Darkly

Gregory C. Gray[1] **and Wu-Chun Cao**[2]

[1]Emerging Pathogens Institute and Department of Environmental and Global Health, College of Public Health and Health Professions, University of Florida, Gainesville; and [2]State Key Laboratory of Pathogen and Biosecurity, Beijing Institute of Microbiology and Epidemiology, People's Republic of China

Keywords. swine influenza; influenza A; zoonoses; infectious disease epidemiology.

First detected in July 2011 [1], the influenza A(H3N2) variant virus (H3N2v), a swine-like progeny virus from the 2009 pandemic H1N1 virus, has caused considerable public health alarm. Most children <10 years of age are thought to be susceptible [2], and evidence of limited H3N2v person-to-person transmission has been reported [1]. Soon after its discovery, public health officials became quite concerned regarding this novel viral threat. In November 2011, the World Health Organization released a virus construct A/Minnesota/11/2010 for vaccine development. In August 2012, the US Centers for Disease Control and Prevention released special H3N2v diagnostic and agricultural fair guidance.

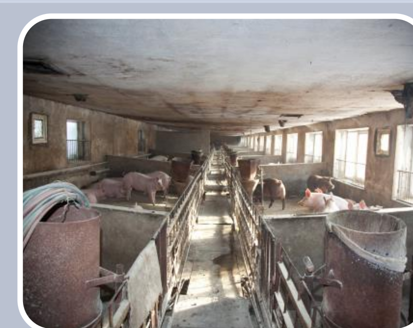
methods and exposure assessments were sound and a number of their findings were quite remarkable: Among the infected persons, 82% were ≤11 years of age, 95% had recent swine exposure, the estimated incubation period was 2.9 days after pig exposure, 16 patients were hospitalized (1 patient died), and 15 likely acquired H3N2v from another human.

Although agricultural fairs have been previously shown to be a risk factor for swine influenza virus (SIV) infections in humans [4–8], never before have the epidemiological data been so strong and geographically widespread. The legion of authors in this paper demonstrates the huge interagency effort that was required to gain such a comprehensive view. The

surveillance programs is for the most part voluntary. Why should the swine industry pay for SIV surveillance and virus characterization among pigs, when pigs often carry influenza A viruses without clinical signs [8] and the viruses are not transmitted to humans via meat products? Unless a novel virus emerges to cause significant morbidity in pigs, and that virus is characterized, the novel virus is not likely to be discovered and reported by veterinary professionals. Lack of SIV ecologic data is also due in part to concerns that research findings might cause economic damage to the pork industries. Why should pork farmers permit researchers to study SIV transmission in their farms when such research could

Zoonotic Swine Influenza Virus Transmission in Confined Animal Feeding Operations NIH R01AI108993

Wu-Chun Cao (Beijing Institute of Microbiology & Epidemiology) and Gregory C. Gray



- Enrollment questionnaire & sera from 300 exposed and 100 nonexposed workers (6 farms)
- Annual serum sampling
- Annual risk factor questionnaire
- Weekly monitoring for ILI & influenza A
- ILI questionnaire
- ILI sera and swabs

- Monthly rope swab sampling of 50 pigs
- Sample various ages (sows, boars, and production pigs)
- 50 pens x 6 farms per month = 300 rope swabs per month

- CAFO questionnaire
- Multiple CAFOs in separate provinces
- Monthly environmental studies of CAFO environment for influenza A
- 144 total aerosol, fecal, environmental swab, and water samples/per month

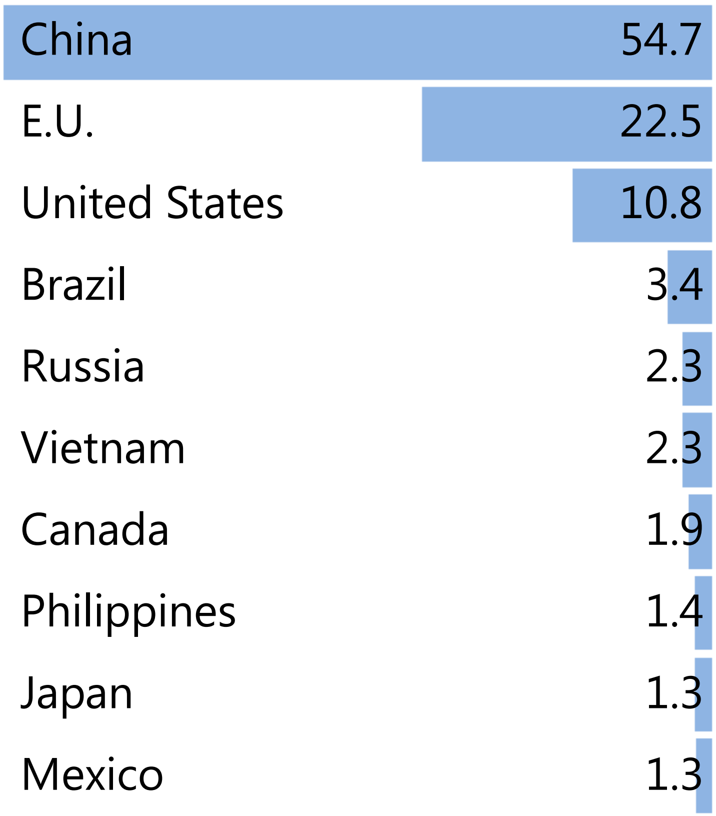
NIH R01AI108993 (2014-2018)

Aims: 1) to identify and characterize enzootic and emergent swine influenza viruses (SIVs), 2) to employ aerosol, fecal, environmental swabs, and water sampling to identify environmental areas with a high prevalence of SIVs, 3) to identify occupational risk factors for SIV infection, and 4) to identify serological and mucosal immunity biomarkers of protection against prevalent and emergent SIVs

China accounts for around ½ of the pork that will be produced and eaten around the world in 2014.[2]

PORK PRODUCTION, 2014

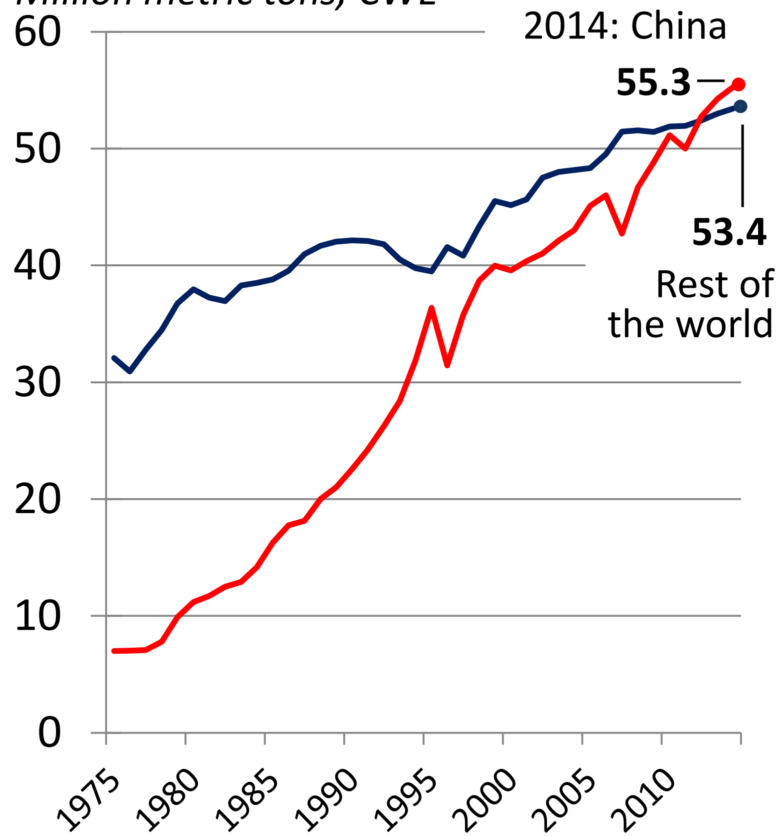
Million metric tons, CWE



Source: U.S. Department of Agriculture, New York Times
Data for 2014 are projected.

PORK CONSUMPTION

Million metric tons, CWE



Source: U.S. Department of Agriculture, New York Times
Data for 2014 are projected.

[1]Hornby, L. (2012, September 10). Bigger Pig Farms Offer China a Way to Calm Pork Prices. *The New York Times*.
[2]Gough, N. (2014, April 10). In I.P.O., a Quest to Satisfy China's Appetite for Pork. *The New York Times*.

China Daily, via Reuters, via the New York Times

From 2010-2012, China's average hog prices were 1.65 times higher than US prices[2]

Why?

- Dependence on small farms for pig production
- High hog feed grain prices
- Reduced amounts of arable land for hog feed due to soil and water pollution and increasing urbanization rates[2]

[1] Hornby, L. (2012, September 10). Bigger Pig Farms Offer China a Way to Calm Pork Prices. *The New York Times*.
[2] Gough, N. (2014, April 10). In I.P.O., a Quest to Satisfy China's Appetite for Pork. *The New York Times*.

Jianan Yu/Reuters, via the New York Times

Large-scale farms with 3000 or more hogs account for only ~2.5% of China's pig production, while large-scale farms account for ~83% of overall US production.[1,2]

In an effort to regulate food cost inflation, Chinese officials support the transition from backyard pig farms to huge industrial farms.[1]

In 2013, China's Shanghui International (now WH Group), the largest pork company in the world, bought out America's largest pork producer, Smithfield Foods, for $4.7 billion hoping to take advantage of the US's lower pork production costs.[2]

WH Group also hopes to improve its Chinese slaughtering plant utilization rates by studying Smithfield's procedures. Last year, its Chinese plants were operating at only 72 percent capacity, while the US based Smithfield plants were operating at 97 percent.

[1]Hornby, L. (2012, September 10). Bigger Pig Farms Offer China a Way to Calm Pork Prices. *The New York Times*.
[2]Gough, N. (2014, April 10). In I.P.O., a Quest to Satisfy China's Appetite for Pork. *The New York Times*.

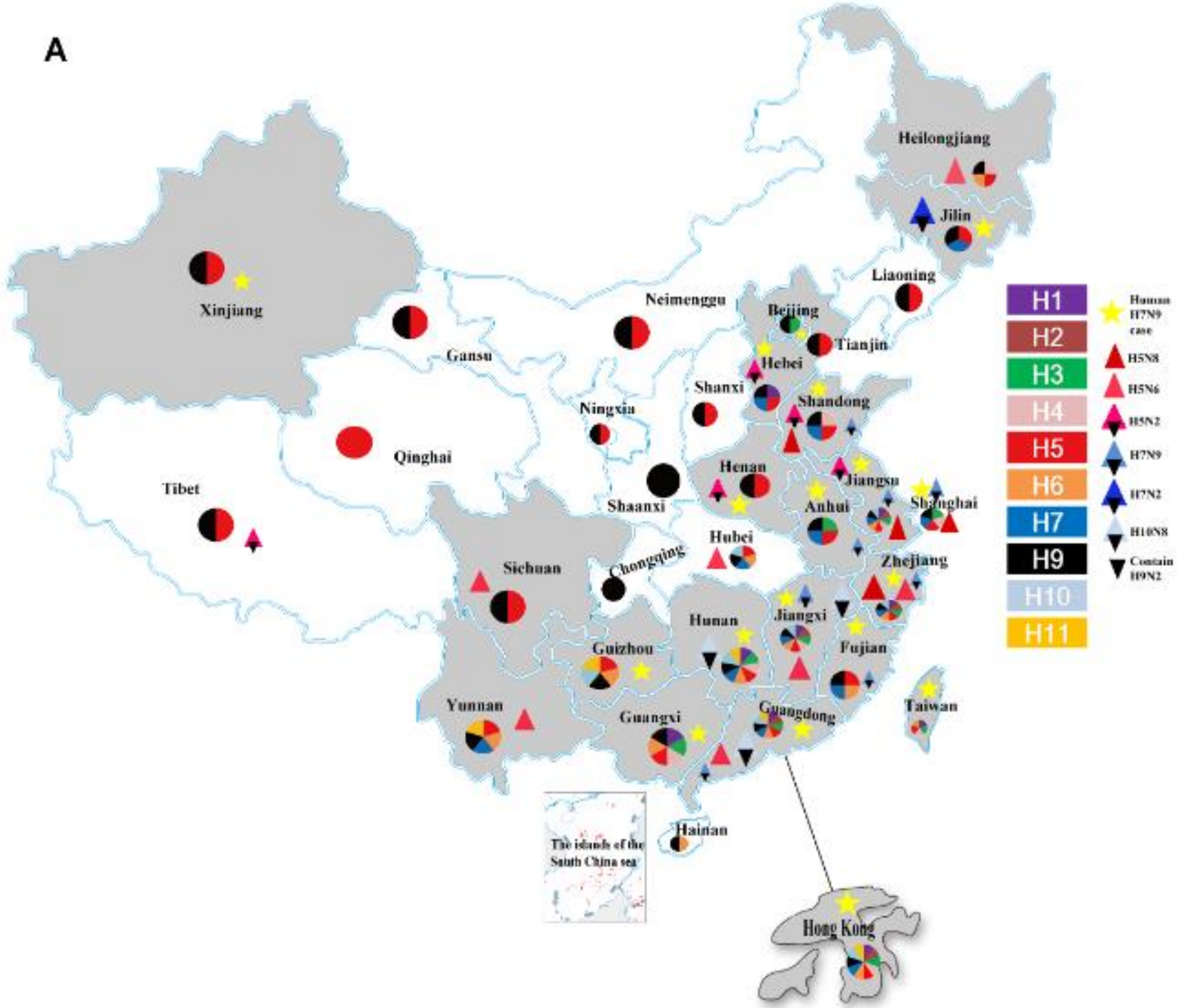
Poor Biosecurity in Confined Animal Feeding Operations

Photo by G.C. Gray 2015

Poor Biosecurity in Confined Animal Feeding Operations

Photos by G.C. Gray 2015

Figure 1. Photographs from a live animal market in Guangdong Province, April 2014, show opportunities for cross-species transfer of pathogens, especially influenza A. Caged cats adjacent caged ducks; geese and chickens in close confinement; chickens caged in close proximity to pigs. Photographs by GCG.

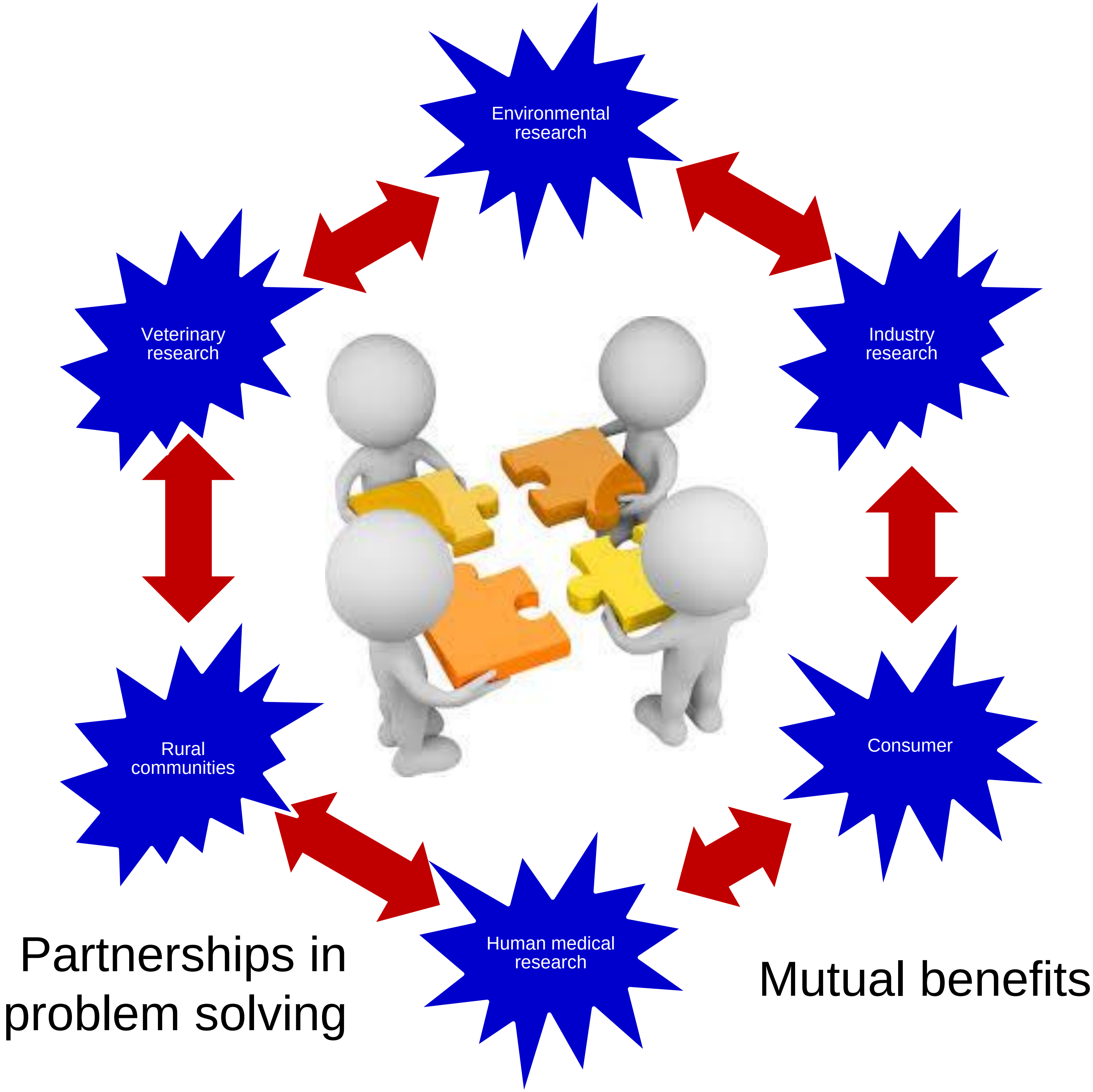


Emergence and distribution of avian influenza viruses in China. Various colors depict different HA subtypes. The gold star indicates human infection with H7N9. The shaded regions represent the emergence of AIV cases in humans. B. A schematic for the emergence of novel AIV in China. The eight bars, from top to bottom, represent the PB2, PB1, PA, HA, NP, NA, M, and NS gene segments. Different colors represent different genetic origins. From: Su S, Bi Y, Bi Y, Wong G, Gray GC, Gao GF, Li S. The epidemiology, evolution and recent outbreaks of avian influenza virus in China: A Review. J Virology 2015; in press

Swine Production Problem?

Human epidemic problem?

National security problem?


Environmental research
Veterinary research
Industry research
Rural communities
Consumer
Human medical research
Partnerships in problem solving
Mutual benefits

Live Animal Markets in Minnesota: A Potential Source for Emergence of Novel Influenza A Viruses and Interspecies Transmission

Mary J. Choi,[1,a] Montserrat Torremorell,[2,a] Jeff B. Bender,[2] Kirk Smith,[3] David Boxrud,[3] Jon R. Ertl,[2] My Yang,[2] Kamol Suwannakarn,[2] Duachi Her,[3] Jennifer Nguyen,[3] Timothy M. Uyeki,[1] Min Levine,[1] Stephen Lindstrom,[1] Jacqueline M. Katz,[1] Michael Jhung,[1] Sara Vetter,[3] Karen K. Wong,[1] Srinand Sreevatsan,[2] and Ruth Lynfield[3]

[1]Centers for Disease Control and Prevention, Atlanta, Georgia; [2]University of Minnesota College of Veterinary Medicine, Minnesota Center of Excellence for Influenza Research and Surveillance, and [3]Minnesota Department of Health, St Paul

Background. Live animal markets have been implicated in transmission of influenza A viruses (IAVs) from animals to people. We sought to characterize IAVs at 2 live animal markets in Minnesota to assess potential routes of occupational exposure and risk for interspecies transmission.

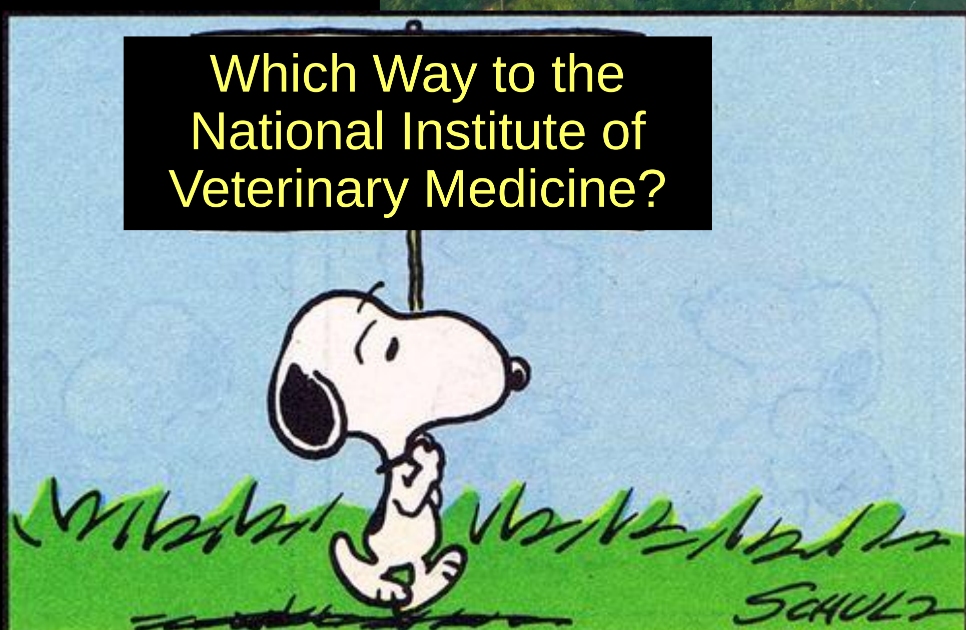
Methods. We implemented surveillance for IAVs among employees, swine, and environment (air and surfaces) during a 12-week period (October 2012–January 2013) at 2 markets epidemiologically associated with persons with swine-origin IAV (variant) infections. Real-time reverse transcription polymerase chain reaction (rRT-PCR), viral culture, and whole-genome sequencing were performed on respiratory and environmental specimens, and serology on sera from employees at beginning and end of surveillance.

Results. Nasal swabs from 11 of 17 (65%) employees tested positive for IAVs by rRT-PCR; 7 employees tested positive on multiple occasions and 1 employee reported influenza-like illness. Eleven of 15 (73%) employees had baseline hemagglutination inhibition antibody titers ≥40 to swine-origin IAVs, but only 1 demonstrated a 4-fold titer increase to both swine-origin and pandemic A/Mexico/4108/2009 IAVs. IAVs were isolated from swine (72/84), air (30/45), and pen railings (5/21). Whole-genome sequencing of 122 IAVs isolated from swine and environmental specimens revealed multiple strains and subtype codetections. Multiple gene segment exchanges among and within subtypes were observed, resulting in new genetic constellations and reassortant viruses. Genetic sequence similarities of 99%–100% among IAVs of 1 market customer and swine indicated interspecies transmission.

Conclusions. At markets where swine and persons are in close contact, swine-origin IAVs are prevalent and potentially provide conditions for novel IAV emergence.

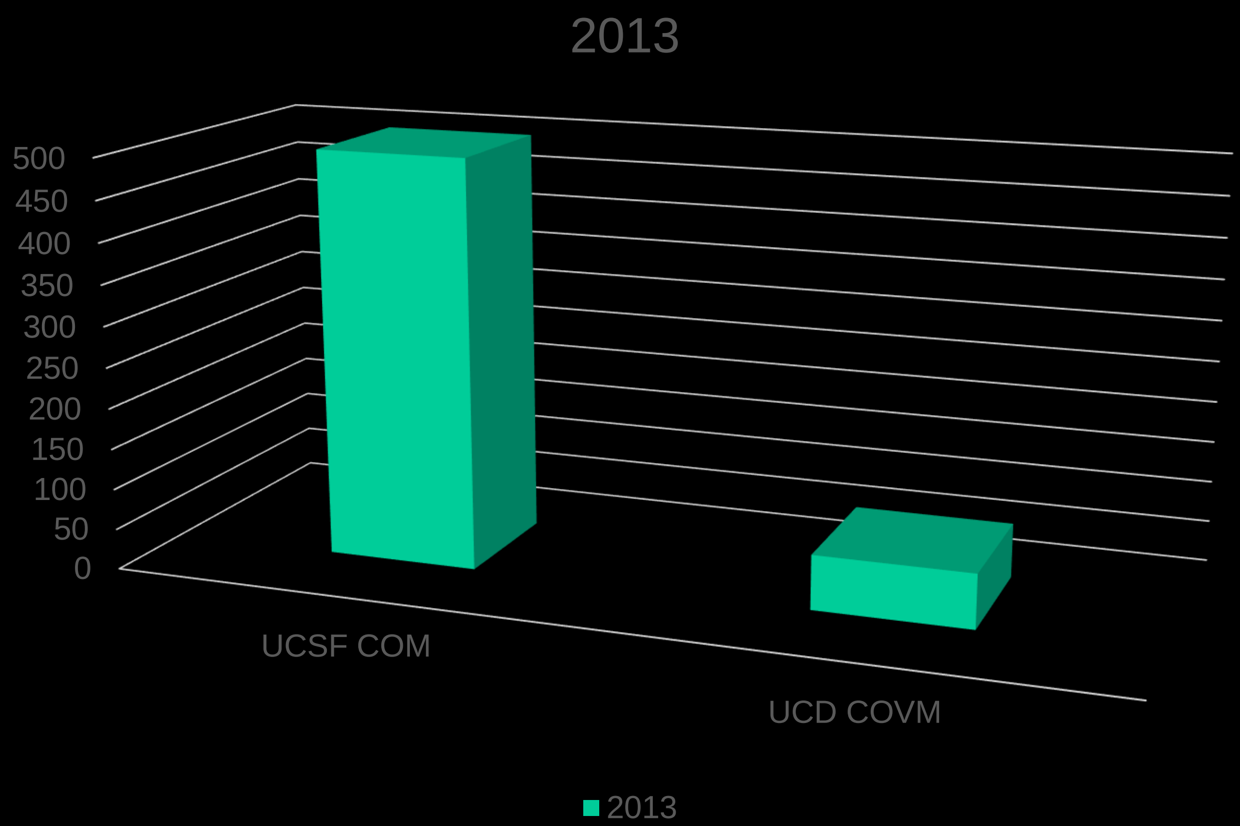
Clinical Infectious Diseases Advance Access published August 17, 2015

Why should agriculture industries partner with other disciplines other than veterinary medicine to study agriculture problems like novel influenza virus emergence?



NATIONAL INSTITUTES OF HEALTH

Estimated UC San Francisco College of Medicine vs. University of California Davis College of Veterinary Medicine Research Funding 2013



New Study Says Bird Flu Spread By Wind, Humans, Fowl

By PEGGY LOWE • JUN 16, 2015

Research shows airborne transmission of avian flu a possibility

By Tom Cherveny on Jun 21, 2015 at 8:30 p.m.

ST. PAUL, Minn. -- Scientists do not yet know whether spring winds carried the highly pathogenic avian influenza into barns and infected turkey or egg-laying flocks.

But they now consider airborne transmission a possibility in some of the cases of infected barns, according to the United States Department of Agriculture. It recently reported that "a preliminary analysis of wind data showed a relationship between sustained high winds and an increase in the number of infected farms approximately five days later."

Signs of airborne H5N2 found; outbreaks

Filed Under: Avian Influenza (Bird Flu)

Robert Roos | News Editor | CIDRAP News | May 08, 2015

Evidence of the H5N2 avian influenza virus has been found in air samples collected in and near infected Minnesota poultry barns, a researcher said today, supporting the suspicion that the virus may go airborne for short distances, while Iowa reported seven new H5 outbreaks involving 4 million chickens and an unknown number of turkeys.

In addition, Wisconsin authorities today reported finding H5N2 in an owl along Green Bay, while hard-hit Minnesota had its second day this week without any new poultry outbreaks.

New Technologies

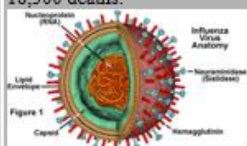
Highly Efficient Collection of Viable Aerosolized Pandemic H1N1 Particles

John Lednicky[1], Maohua Pan[2], Julia Loeb[1], Hsin Hsieh[3], Arantzazu Eiguren-Fernandez[4], Susanne Hering[4], Chang-Yu Wu[2], Hugh Fan[5], Nima Afshar-Mohajer [2, 6]

[1]Department of Environmental and Global Health, University of Florida, Gainesville, FL, USA [2]Department of Environmental Engineering Sciences, University of Florida, Gainesville, FL, USA [3]Department of Microbiology and Cell Science, University of Florida, Gainesville, FL, USA [4]Aerosol Dynamics Inc., Berkeley, CA, USA USA [5]Department of Mechanical and Aerospace Engineering, University of Florida, Gainesville, FL, USA [6]Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA

BACKGROUND

• Influenza is one of the most contagious respiratory diseases and an important cause of morbidity, hospital admissions and mortality.
• In 2009, a pandemic caused by a new H1N1 strain resulted in 43 – 89 million people infected and up to 18,300 deaths.



• Transmission of influenza virus between humans mainly occurs by three routes: direct or indirect contact, large droplet spray, aerosolized viruses.
• Existing samplers have low efficiency (5-10%) in collecting virus aerosols in the range of 20 - 300 nm[1].

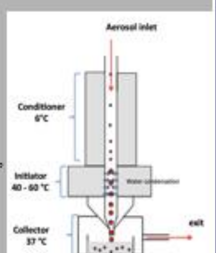
OBJECTIVES

• Evaluate the performance of the Super Efficient Sampler for Influenza virus (SESI), based on ~~the~~ water condensation particle growth technology, in amplifying virus aerosols to larger size for improved physical and viable collection efficiency.

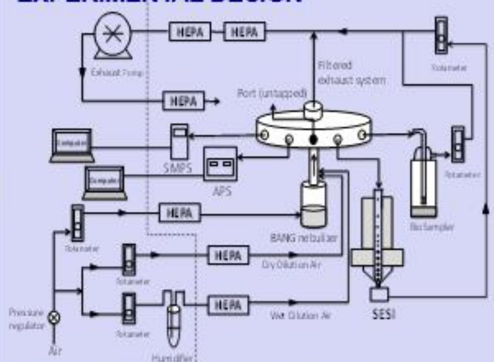
METHODS

• Influenza virus strain A/Mexico/4108/2009 (pH1N1) (A/Mex) was obtained as a low-passage stock and propagated in MDCK cells in serum-free aDMEM with TPCK-trypsin with incubation at 5% CO2 and 33 °C [2].

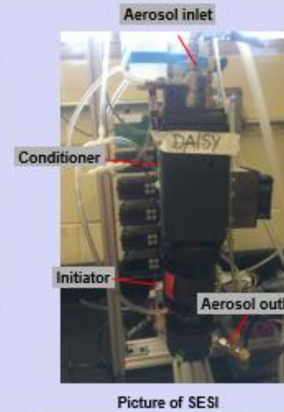
• Condensation was used to enlarge influenza virus particles by introducing aerosols into a "growth tube" with a wetted wall held at higher temperature[3].



EXPERIMENTAL DESIGN



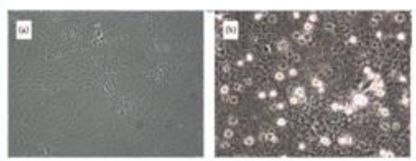
Schematic diagram of the system used to collect Influenza virus



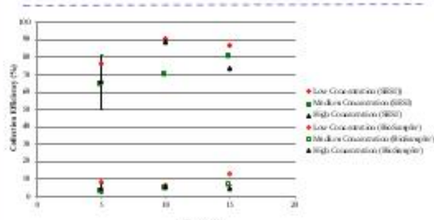
Picture of SESI

RESULTS

Early formation of influenza virus-specific CPE in cells



(a) Noninfected ATCC MDCK cells (negative control, 3 days postseed)
(b) ATCC MDCK cells inoculated with influenza virus



Viable influenza virus collection efficiency of SESI as a function of different collection time and concentration

Viability number

✓Viable collection efficiency of SESI (77.5 ± 9.4)% vs BioSampler (6.5 ± 2.8)%.

✓No significant collection efficiency difference for different starting concentrations and different collection times.

✓For collection times ranging from 5 min to 15 min, the viable H1N1 captured by the SESI was averaged 12 times higher than for the BioSampler, with inferred airborne concentrations of 4200±380 viruses/L of air as compared with 470±160 viruses/L for the BioSampler.

✓ Fabian P et al[5] compared the collection performance of an SKC Biosampler, a compact cascade impactor (CCI), Teflon filters, and gelatin filters, and found out that the SKC BioSampler recovered and preserved influenza virus infectivity much better than the other samplers. They also state that a new sampler is need for virus aerosol sampling.

✓ McDevitt J. et al[6] built a system and found that it had a performance "comparable" to the BioSampler.

CONCLUSIONS

• The SESI efficiency for viable H1N1 capture is 12 times higher than that of the BioSampler.
• Water condensational particle growth technology significantly increases the collection efficiency of viable influenza H1N1. It achieves this by amplifying the diameter of aerosolized virus particles while minimizing damages/inactivation of the virus particles

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ACKNOWLEDGEMENT

We would like to thank National Science Foundation (NSF) and Aerosol Dynamics Inc for supporting this research (Grant number: IDBR-1353423). Any opinions, findings, and conclusions or recommendations expressed in this material are those of the authors and do not necessarily reflect the views of the National Science Foundation.

How can we operationalize the One Health approach?

SESSION FOUR: Successful Approaches or Systems for Implementing One Health—Examples From Other Sectors (Professional, NGO, International, and Academia)

Examples of behaviors that can prevent progress, how they were identified as the root factor, and how political will was engaged to implement One Health were presented and discussed. Examples of behavioral changes leading to sustainable change were also discussed.

Panel: John Mackenzie, Curtin University of Technology, Laura Kahn, Princeton University, Manish Kakkar, Public Health Foundation of India, Roland Suluku, Animal Health Clubs (Sierra Leone)

SESSION FIVE: Creating a Shared View of Success for One Health

Panelists shared their own ideas of success for One Health in terms of outcomes and benefits in order to create a collective view for the group.

Panel: Lonnie King, The Ohio State University, Jian Du, China Ministry of Agriculture, John McDermott, International Livestock Research Institute


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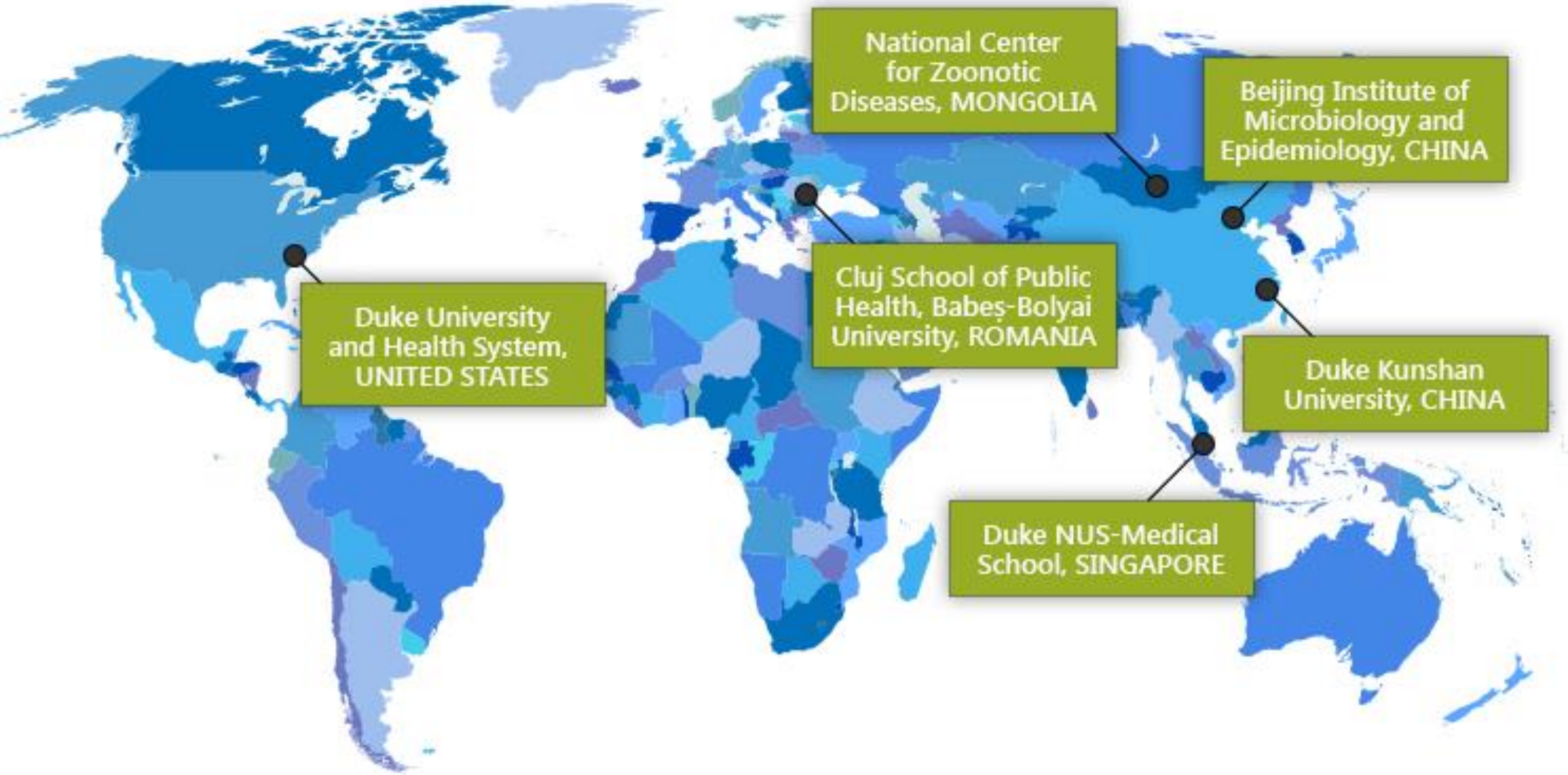

Image created by Anastasia Lambrou